



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 133469

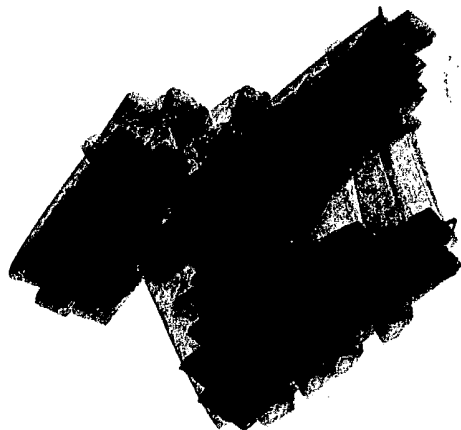
TO: James Schultz
Location: REM/2D18/2C18
Art Unit: 1635
Thursday, September 23, 2004

Case Serial Number: 09/227881

From: David Schreiber
Location: Biotech-Chem Library
Remsen E01A61
Phone: 272-2526

david.schreiber@uspto.gov

Search Notes



This Page Blank (uspto)

Schreiber, David

133469

From: Schultz, James
Sent: Tuesday, September 14, 2004 11:30 AM
To: Schreiber, David
Subject: RE: Seq Search 09/227,881

OK, just run it on the full length SEQ Id NO:3.
thanks,
Doug

-----Original Message-----

From: Schreiber, David
Sent: Tuesday, September 14, 2004 11:21 AM
To: Schultz, James
Subject: RE: Seq Search 09/227,881

Doug,

Seq3 is only 6169 residues long. It doesn't make sense to run a separate search for the fragment in score over length when the fragment is so close in length to the full length sequence.

David Schreiber, Ph.D.
Scientific and Technical Information Center
Biotech/Chem Library
Old address and phone:
CM1-6A03
703-308-4292
New address and phone:
Remsen E01A61
571-272-2526

-----Original Message-----

From: Schultz, James
Sent: Tuesday, September 14, 2004 11:16 AM
To: Schreiber, David
Subject: Seq Search 09/227,881

Hi David,

Could you please run a score over length nucleotide sequence search on nucleotides 1 through 5271, and also on the full length of SEQ ID NO:3 in the above entitled case, which returns hits between 12 and 250 nucleotides long? Please transfer in as many hits as possible, but only include those that are 100% identical to the target. Please include the interference databases as well.

Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 09:55:27; Search time 7 Seconds
(without alignments)
3.592 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169
Sequence: 1 attcttggtcagttacatc.....cttggtccctccatgctcag 6169

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 76 seqs, 2038 residues

Total number of hits satisfying chosen parameters: 152

Minimum DB seq length: 12

Maximum DB seq length: 250

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 77 summaries

Database: rng3.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the local score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	3.7	227	1 AA57515	Triabecular meshwor
2	29	0.5	29	1 AA237976	GLCIA coding seque
3	28	0.5	28	1 AAQ33645	Microsatellite seq
4	28	0.5	28	1 AAQ34161	Sequence of a micr
5	28	0.5	28	1 AAQ34035	Microsatellite seq
6	28	0.5	28	1 AA66102	Repeat sequence fo
7	27	0.4	27	1 AAQ34044	Microsatellite seq
8	27	0.4	27	1 AAQ33678	Microsatellite seq
9	27	0.4	27	1 AAQ33804	Microsatellite seq
10	27	0.4	27	1 AAQ34181	Microsatellite seq
11	27	0.4	27	1 AAQ34012	Microsatellite seq
12	27	0.4	27	1 AAQ34143	Sequence of a micr
13	27	0.4	27	1 AAQ33951	Oligonucleotide cl
14	27	0.4	27	1 AA65733	Repeat sequence fr
15	27	0.4	27	1 AAH24300	Synthetic antineop
16	27	0.4	27	1 AAH46017	Synthetic oligonuc
17	27	0.4	27	1 AAH46001	Synthetic oligonuc
18	27	0.4	27	1 AAH46005	Oligonucleotide cl
19	27	0.4	27	1 AA660473	Oligonucleotide cl
20	26	0.4	26	1 AAQ34083	Microsatellite seq
21	26	0.4	26	1 AAQ33684	Microsatellite seq
22	26	0.4	26	1 AAQ33704	Microsatellite seq
23	26	0.4	26	1 AAQ33831	Microsatellite seq
24	26	0.4	26	1 AAQ33837	Microsatellite seq
25	26	0.4	26	1 AAQ36250	Human glaucoma dia
26	25	0.4	25	1 AAQ33918	Microsatellite seq
27	25	0.4	25	1 AAQ33642	Microsatellite seq
28	25	0.4	25	1 AAQ33962	Microsatellite seq
29	25	0.4	25	1 AAQ33861	Microsatellite seq
30	25	0.4	25	1 AAH5734	Repeat sequence fr
31	25	0.4	25	1 AAH40163	SNP specific SNPE
32	25	0.4	25	1 AAH38303	SNP specific SNPE
33	25	0.4	25	1 AAH96251	Human glaucoma dia

34	24	0.4	24	1 AAQ33986	Microsatellite seq
35	24	0.4	24	1 AAQ34158	Sequence of a micr
36	24	0.4	24	1 AAQ33909	Microsatellite seq
37	24	0.4	24	1 AAQ34065	Microsatellite seq
38	24	0.4	24	1 AAQ34024	Microsatellite seq
39	24	0.4	24	1 AAQ33707	Microsatellite seq
40	24	0.4	24	1 AA66095	Repeat sequence fo
41	24	0.4	24	1 AAH46015	Synthetic oligonuc
42	24	0.4	24	1 AAH46016	Synthetic oligonuc
43	24	0.4	24	1 AAQ33885	Arginogenesis inhib
44	24	0.4	24	1 AB878584	Human RNA polymera
45	24	0.4	24	1 AB870110	Immunostimulatory
46	24	0.4	24	1 ACH03377	Immunostimulatory
47	24	0.4	24	1 AD337364	Microsatellite seq
48	24	0.4	24	1 AAQ33863	Microsatellite seq
49	23	0.4	23	1 AAQ33773	Microsatellite seq
50	23	0.4	23	1 AAQ33885	Repeat sequence fo
51	23	0.4	23	1 AA66105	Oligonucleotide cl
52	23	0.4	23	1 AA660472	Triabecular meshwor
53	22.4	0.4	227	1 AA57515	Microsatellite seq
54	22	0.4	22	1 AAQ33810	Microsatellite seq
55	22	0.4	22	1 AAQ33675	Microsatellite seq
56	22	0.4	22	1 AAQ34038	Microsatellite seq
57	22	0.4	22	1 AAQ34080	Microsatellite seq
58	22	0.4	22	1 AAQ33991	Microsatellite seq
59	22	0.4	22	1 AAQ83952	Oligonucleotide cl
60	22	0.4	22	1 AA65727	Repeat sequence fr
61	22	0.4	22	1 AA64448	SSR motif #8. Uni
62	22	0.3	22	1 AAQ33891	Microsatellite seq
63	21	0.3	21	1 AAQ34015	Microsatellite seq
64	21	0.3	21	1 AAQ33879	Microsatellite seq
65	21	0.3	21	1 AAQ90296	Oligonucleotide RT
66	21	0.3	21	1 AA65738	Repeat sequence fr
67	21	0.3	21	1 AA51377	Human TIGR PCR pri
68	21	0.3	21	1 AA51373	Human TIGR PCR pri
69	21	0.3	21	1 AA51795	Primer used for SS
70	21	0.3	21	1 AA57491	Synthetic oligonuc
71	21	0.3	21	1 AAH46013	Synthetic oligonuc
72	21	0.3	21	1 AAH46014	Immunostimulatory
73	21	0.3	21	1 AA69702	Arginogenesis inhib
74	21	0.3	21	1 AB878423	IFNARI forward PCR
75	21	0.3	21	1 ACR64053	Immunostimulatory
76	21	0.3	21	1 ACH03241	Immunostimulatory
77	21	0.3	21	1 ADB37204	Immunostimulatory

ALIGNMENTS

RESULT 1	
ID AA57515	AA57515 standard; DNA; 227 BP.
AC AA57515;	
DT 20-OCT-2000	(first entry)
XX	
DE	Triabecular meshwork inducible glucocorticoid receptor gene fragment.
XX	
KW	TIGR; triabecular meshwork inducible glucocorticoid receptor; promoter;
KM	glaucoma; steroid sensitivity; progressive ocular hypertension;
XX	vision loss; ss.
OS	Homo sapiens.
XX	
PN	W0200042220-A1.
XX	
PD	20-JUL-2000.
XX	
PF	11-JAN-2000; 2000NC-US000559.
XX	
PR	11-JAN-1999; 99US-00227881.
PR	07-MAY-1999; 99US-00306828.

XX (REGC) UNIV CALIFORNIA.
 XX PA
 XX NGuyen TD, Polansky JR, Chen P, Chen H;
 PI WPI; 2000-491060/43.
 XX
 DR
 PT Diagnosis, prognosis and treatment of glaucoma, based on detecting
 PT specific polymorphisms in the promoter of the trabecular meshwork
 PT inducible glucocorticoid receptor gene.
 XX
 PS Claim 90; Page 119; 122pp; English.
 XX
 CC The present sequence represents a fragment of a TIGR (trabecular meshwork
 CC inducible glucocorticoid receptor) gene. The specification describes a
 CC method for the diagnosis, prognosis and treatment of glaucoma, based on
 CC detecting specific polymorphisms in the promoter of the TIGR gene. The
 CC method is used for diagnosis and prognosis of glaucoma (of all types),
 CC steroid sensitivity and progressive ocular hypertension that leads to
 CC loss of vision. Glaucoma can be treated by administering an agent that
 CC binds to cis-acting elements within the TIGR promoter. The TIGR promoter
 CC (or other regulatory regions) can be used to express homologous or
 CC heterologous genes, particularly for tissue-specific expression of
 CC therapeutic transgenes for treating glaucoma, also to generate transgenic
 CC animals and in screening for compounds (specific modulators) with
 CC diagnostic or therapeutic potential. Fragments of the TIGR sequence can
 CC be used as amplification primers or probes, e.g. for isolating related
 CC sequences in non-human animals
 XX
 SQ Sequence 227 BP; 57 A; 61 C; 53 G; 56 T; 0 U; 0 Other;
 XX
 Query Match 3.7%; Score 227; DB 1; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.9e-15;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 5045 AACTATTATTGGGGTATGGGTCATTAATTTGGATGTTCTTTTAAAGAACTCCAAA 5104
 DB 1 AACTATTATTGGGGTATGGGTCATTAATTTGGATGTTCTTTTAAAGAACTCCAAA 60
 XX
 QY 5105 CAGACTCTGGAAGGTTATTTCTTGAAGATCTGCTGACAGGGAAGCAACCCCTG 5164
 DB 61 CAGACTCTGGAAGGTTATTTCTTGAAGATCTGCTGACAGGGAAGCAACCCCTG 120
 XX
 QY 5165 TGGACAGCCCAACCAAGCCTCACTGCGCACTCTGTTCCCAATGAAGGCTGCTC 5224
 DB 121 TGGACAGCCCAACCAAGCCTCACTGCGCACTCTGTTCCCAATGAAGGCTGCTC 180
 XX
 QY 5225 CCGAGTATATTAACCTCTCTGAGCTCGGGGCAAGACCGCAAGG 5271
 DB 181 CCGAGTATATTAACCTCTCTGAGCTCGGGGCAAGACCGCAAGG 227
 XX
 RESULT 2
 AA237976
 ID AA237976 standard; DNA; 29 BP.
 AC AA237976;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE GLCIA coding sequence fragment (basepair 344-372).
 XX
 KW Glaucoma; PCR amplification; primary open wide angle glaucoma;
 KW GLCIA gene; human; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO9951779-A2.
 XX
 PD 14-OCT-1999.
 XX
 PF 07-APR-1999; 99WO-US007671.
 XX

PR 07-APR-1999; 98US-00056285.
 XX
 XX (IOWA) UNIV IOWA RES FOUND.
 XX PA
 XX Stone EM, Sheffield VC, Alward WM, Fingert J;
 PI WPI; 2000-022956/02.
 XX
 DR
 PT Determination of a predisposition to glaucoma by analysing mutations in
 PT the GLCIA gene.
 XX
 PS Disclosure; Page 14; 137pp; English.
 XX
 CC The invention relates to a method for the determination of a
 CC predisposition to glaucoma. The method comprises amplifying a GLCIA gene
 CC with a primer pair selected from the sequences shown in AA237981-238008.
 CC The primers are used to determine whether a subject has or has the
 CC potential to develop primary open wide angle glaucoma. The present
 CC sequence represents the human GLCIA coding sequence fragment (basepair
 CC 344-372), which is not included in the TIGR sequence
 XX
 SQ Sequence 29 BP; 5 A; 7 C; 14 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.5%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 5680 AGGGGCTGCAAGAGGAGCTGGGCAACCTG 5708
 DB 1 AGGGGCTGCAAGAGGAGCTGGGCAACCTG 29
 XX
 RESULT 3
 AAQ33645
 ID AAQ33645 standard; DNA; 28 BP.
 AC AAQ33645;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone MTG73.
 XX
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 PN WO9213102-A1.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US000340.
 XX
 PR 15-JAN-1991; 91US-00642342.
 XX
 XX (GENM-) GENMARK.
 XX
 PA Georges M. Massey JM;
 XX
 PI WPI; 1992-284684/34.
 XX
 DR
 PT Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX
 PS Table 7; Page 187; 517pp; English.
 XX
 CC The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (76)n >9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information

CC breeding. See also AQ33501-34437. (updated on 25-MAR-2003 to correct PR field.)

Query Match	0.5%;	Score 28;	DB 1;	Length 28;
Best Local Similarity	100.0%;	Pred. No. 12;		
Matches 28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Query Match	0.5%;	Score 28;	DB 1;	Length 28;
Best Local Similarity	100.0%;	Pred. No. 12;		
Matches 28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

ID	AAT66102 standard; DNA; 28 BP.
AC	AAT66102;
DT	25-MAR-2003 (revised)
DT	18-JUN-1997 (first entry)
DE	Repeat sequence found in the human chromosomal clone SW10.
KM	Polymorphism; repeat sequence; genetic marker; primer; amplification;
KM	PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KM	linkage analysis; genetic disease; animal; plant; breeding; locus;
KM	hybridisation; chromosome; ds.
OS	Homo sapiens.
XX	
PN	USS582979-A.
PD	10-DEC-1996.
XX	
PF	04-APR-1994; 94US-00222177.
XX	
PR	21-APR-1989; 89US-00341562.
PR	05-SEP-1991; 91US-00754351.
PA	(MAR-) MARSHFIELD CLINIC.
PI	Weber JL;
DR	WPI; 1997-042299/04.
PT	Detection of polymorphic genetic markers of the form (dc-da)n(dg-dt)n -
PS	using novel nucleic acid mols. as primers.
XX	
XX	Example 9; Col 61-62; 18bp; English.
CC	The invention relates to the isolation of polymorphic repeat sequences
CC	having the sequence (dc-da)n.(dg-dt)n which can be used as genetic
CC	markers. Primers based on these sequences can be used to detect these
CC	repeats, especially for use in e.g. paternity or maternity testing, human
CC	animal or plant breeding or pedigree analysis. The sequences AAT66084-
CC	T66107 represent repeat sequences of low informativeness found in
CC	specific human genes. This repeat sequence is found in the human
CC	chromosomal clone SW10. The sequence is amplified by primers AAT6103-4,
CC	(updated on 25-MAR-2003 to correct pf field.)
SQ	Sequence 28 BP, 14 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
Query Match	0.5%; Score 28; DB 1; Length 28;
Best Local Similarity	100.0%; Pred.No.12;
Matches 28; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	4996 GTGTGTTGTGTGTGTGTGTGTGTGTGT 5023
DB	28 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1
RESULT 7	
ID	AAQ34044
AC	AAQ34044 standard; DNA; 27 BP.
XX	
XX	AAQ34044;
XX	
DT	25-MAR-2003 (revised)
DT	02-FEB-1993 (first entry)
DE	Microsatellite sequence from clone TGLA435.
XX	

KW	PCR; selection; primers; OPTIRIM; breeding; cattle; parentage;
XV	genetic mapping; traits; amplification; ss.
XX	
OS	Bos taurus.
XX	
FN	MO92J1102-A1.
PD	06-AUG-1992.
XX	
PF	15-JAN-1992; 92MO-US000340.
XX	
FR	15-JAN-1991; 91US-00642342.
PA	(GENM-) GENMARK.
PI	Georges M, Massey JW;
DR	WPI; 1992-284684/34.
XX	
PT	Polymorphic bovine DNA markers - used in genetic identification, gene
XX	mapping, and selective breeding.
PS	Table 7, Page 348; 517pp: English.
XX	
CC	The sequence is that of a bovine microsatellite sequence obtd. by
CC	screening a library of bovine MboI DNA fragments of between 250 and 500
CC	bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC	clones cross-hybridised. Assuming independent distribution of
CC	microsatellites and MboI sites, the frequency of (T)n >9 microsatellites
CC	in the bovine genome is estimated at >100,000. The sequence information
CC	for ca. 230 such bovine microsatellites is summarised in the
CC	specification and indexed herein (see below). The sequences upstream and
CC	downstream of the microsatellite sequence were used to generate the
CC	required PCR primers for in vitro amplification of the corresp.
CC	microsatellite (using the program OPTIRIM). The microsatellites may be
CC	used to identify individuals, for parentage testing, and in the genetic
CC	mapping of economic trait loci, or genes involved the determination of
CC	economically important traits esp. in cattle, to allow selective
CC	breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC	field.)
SQ	Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
XX	
XX	Query Match 0.4%; Score 27; DB 1; Length 27;
XX	Best Local Similarity 100.0%; Pred. No. 14;
XX	Matches 27; Conservative * 0; Mismatches 0; Indels 0; Gaps 0
CY	4997 TCGTGCTGCTGCTGCTGCTGCTGCTGCT 5023
DB	1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27
DE	RESULT 8
XX	AAQ33678
XX	AAQ33678 standard; DNA; 27 BP.
XX	AAQ33678;
XX	
DT	25-MAR-2003 (revised)
DT	02-FEB-1993 (first entry)
DE	Microsatellite sequence from clone TGLA12.
XX	
XX	PCR; selection; primers; OPTIRIM; breeding; cattle; parentage;
XX	genetic mapping; traits; amplification; ss.
OS	Bos taurus.
XX	
PN	MO92J1102-A1.
PD	06-AUG-1992.
PF	15-JAN-1992; 92MO-US000340.

XX 15-JAN-1991; 91US-00642342.
 PR (GENM-) GENMARK.
 XX Georges M, Massey JM;
 PI WPI; 1992-284684/34.
 XX
 PT Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX Table 7; Page 201; 517pp; English.
 PS
 CC The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)_n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 XX
 SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
 Query Match 0.4%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5023
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27
 RESULT 9
 AAQ33804
 ID AAQ33804 standard; DNA; 27 BP.
 XX
 AC AAQ33804;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA210.
 XX
 KM PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KM Genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 PN WO9213102-A1.
 PN
 PD 06-AUG-1992.
 PD
 PF 15-JAN-1992; 92WO-US000340.
 PF
 PR 15-JAN-1991; 91US-00642342.
 PR
 PA (GENM-) GENMARK.
 PA
 PI Georges M, Massey JM;
 PI
 DR WPI; 1992-284684/34.
 DR
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT

PT mapping, and selective breeding.
 XX
 PS Table 7; Page 251; 517pp; English.
 PS
 CC The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)_n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 XX
 SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
 Query Match 0.4%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5023
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27
 RESULT 10
 AAQ34181
 ID AAQ34181 standard; DNA; 27 BP.
 XX
 AC AAQ34181;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA98.
 XX
 KM PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KM Genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 PN WO9213102-A1.
 PN
 PD 06-AUG-1992.
 PD
 PF 15-JAN-1992; 92WO-US000340.
 PF
 PR 15-JAN-1991; 91US-00642342.
 PR
 PA (GENM-) GENMARK.
 PA
 PI Georges M, Massey JM;
 PI
 DR WPI; 1992-284684/34.
 DR
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 XX mapping, and selective breeding.
 XX Table 7; Page 403; 517pp; English.
 PS
 CC The sequence is a bovine microsatellite sequence obtd. by screening a
 CC library of bovine MboI DNA fragments of between 250 and 500 bp with an
 CC (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50 clones cross-
 CC hybridised. Assuming independent distribution of microsatellites and MboI
 CC sites, the frequency of (T6)_n > 9 microsatellites in the bovine genome is
 CC estimated at >100, 000. The sequence information for ca. 230 such bovine

KW		immunosensitisation reduction; cancer; tumour; cytosstatic; ss.
XX	SS	Synthetic.
XX	PN	WO200147561-A1.
XX	PD	05-JUL-2001.
XX	PF	28-DEC-2000; 2000WO-CA001562.
XX	PR	28-DEC-1999; 99US-0173375P.
XX	PA	(BION-) BIONICHE LIFE SCI INC.
XX	PI	Phillips NC, Filion MC;
XX	DR	WPI; 2001-408766/43.
PT		Synergistic compositions comprising hyaluronic acid and Mycobacterium
PT		phlei DNA and cell walls, useful for treating cancers.
XX		
PS		Example 7, Page 23, 27pp; English.
XX		
CC		The invention relates to compositions for the treatment of cancers,
CC		comprising purified hyaluronic acid (HA) and a second antineoplastic
CC		agent such as Mycobacterium phlei DNA, a Mycobacterium phlei DNA/cell
CC		wall complex, a cytotoxic chemotherapeutic drug or a synthetic
CC		antineoplastic oligonucleotide. On its own, HA stimulates the production
CC		of the cytokines interleukin-6 (Il-6) and Il-12 by immune system cells.
CC		In combination, HA and the second antineoplastic agent of the composition
CC		act synergistically to potentiate each other's ability to inhibit
CC		proliferation and induce apoptosis in cancer cells. Due to the synergy
CC		between the HA and the second antineoplastic agent, a reduced standard
CC		dose of the second antineoplastic agent can be used without compromising
CC		the therapeutic effectiveness of the cancer treatment. The reduction in
CC		dose helps to reduce adverse side-effects and the development of drug
CC		resistance or immunosensitisation, thereby improving the quality of life
CC		for the patient. In addition, as HA is inexpensive and as most
CC		chemotherapeutic drugs are expensive, the combined use of HA and a
CC		chemotherapeutic drug can significantly reduce the cost of cancer
CC		treatment. The increase in dose effectiveness, decrease in toxicity and
CC		decrease in cost address provide important benefits for mammals,
CC		including humans. The present sequence represents a synthetic
CC		antineoplastic oligonucleotide which was used in a composition with HA in
CC		an exemplification of the invention
XX		
SO		Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
		Query Match 0.4%; Score 27; DB 1; Length 27;
		Best Local Similarity 100.0%; Pred. No. 14;
		Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY		4996 GTGTGTCGTGTCGTGTCGTGTCGTG 5022
DB		1 GTCTGTCTGTCTGTCTGTCTGTCTGTG 27
RESULT 16		
ID	AAH46017	
AC	AAH46017	standard; DNA; 27 BP.
DE	12-SEP-2001	(first entry)
XX		Synthetic oligonucleotide 17.
XX		
KW		Synthetic oligonucleotide; dinucleotide repeat; cytosstatic; apoptosis;
KW		cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
KW		tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
KW		Lymphoma; ss.
XX		Synthetic.

[illegible]

[illegible]

	DR	WT1; 2001-798150/42.
CC	PT	Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating caspases.
XX	PS	Example 4; Page 16; 77pp; English.
XX	CC	The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TC, etc., according to specific formulae and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as leukaemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/Cip, p15(Ink4B), p16(Ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone dependence
SQ	Sequence	27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
CY	Query Match 0.4%; Score 27; DB 1; Length 27; Best Local Similarity 100.0%; Pred. No. 14; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
DB	1	TGTCGTCTGTCGTCTGTCGTCTGTCGT TGTCGTCTGTCGTCTGTCGTCTGTCGT 5023
RESULT 19	AAP60473/c	ID AAP60473 standard; DNA; 27 BP.
AC	AAP60473;	
DT	27-APR-2001	(first entry)
DE	Oligonucleotide clamp #19.	
KM	Oligonucleotide clamp; ds.	
OS	Unidentified.	
PN	US6180777-B1.	
PD	30-JAN-2001.	
PF	03-JAN-1997;	97US-00787321.
PR	12-JAN-1996;	96US-000991BP.
PA	(PARB) BAYER CORP.	
PI	Horn T;	
WI	WPI; 2001-201911/20.	
XX	PT	Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having halobutylamino groups and second units having thiol or phosphorothioate groups.
XX	Disclousure;	Col 29-30; 20pp; English.
XX	CC	The present invention relates to a method for synthesising a branched or multiply connected macromolecular structure, comprising oligonucleotide clamps (OC). The macromolecular structure is capable of specifically

XX	Claim 6, Page 21, 26pp; Japanese.
PS	
CC	The invention relates to a polynucleotide (AB96248) useful for pre-
CC	diagnosing glaucoma. The present sequence is that of a glaucoma diagnosis
CC	related PCR primer of the invention
CC	
XX	Sequence 26 BP, 11 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
SO	
QY	Query Match 0.4%; Score 26; DB 1; Length 26;
	Best Local Similarity 100.0%; Pred. No. 17;
	Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 GTAAACCGAGTGGAGTATTGGAAC 5047
	1 GTAAACCGAGTGGAGTATTGGAAC 26
RESULT 26	
AA033918	
ID	AA033918 standard; DNA, 25 BP.
XX	
AC	AA033918;
XX	
DT	25-MAR-2003 (revised)
DT	02-FEB-1993 (first entry)
XX	
DE	Microsatellite sequence from clone TGLA327.
XX	
KW	PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW	genetic mapping; traits; amplification; ss.
XX	
OS	Bos taurus.
XX	
PN	MO9213102-A1.
PD	
XX	06-AUG-1992.
XX	
PF	15-JAN-1992; 92WO-US000340.
XX	
PR	15-JAN-1991; 91US-00642342.
XX	
PA	(GENM-) GENMARK.
XX	
PI	Georges M, Massey JM;
XX	
DR	WPI, 1992-284684/34.
XX	
PT	Polymorphic bovine DNA markers - used in genetic identification, gene
XX	mapping, and selective breeding.
XX	
PS	Table 7; Page 297; 517pp; English.
XX	
CC	The sequence is that of a bovine microsatellite sequence obd. by
CC	screening a library of bovine MboI DNA fragments of between 250 and 500
CC	bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC	clones cross-hybridised. Assuming independent distribution of
CC	microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC	in the bovine genome is estimated at >100, 000. The sequence information
CC	for ca. 230 such bovine microsatellites is summarised in the
CC	specification and indexed herein (see below). The sequences upstream and
CC	downstream of the microsatellite sequence were used to generate the
CC	required PCR primers for in vitro amplification of the corresp.
CC	microsatellite (using the program OPTIPRIM). The microsatellites may be
CC	used to identify individuals, for parentage testing, and in the genetic
CC	mapping of economic trait loci, or genes involved the determinism of
CC	economically important traits esp. in cattle, to allow selective
CC	breeding. See also AA033501-34437. (Updated on 25-MAR-2003 to correct PN
CC	field.)
XX	
QX	Sequence 25 BP, 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
Query Match	0.4%; Score 25; DB 1; Length 25;

[illegible]

XX	DE	Microsatellite sequence from clone TGLA444.
XX	KM	PCR; selection; primers; OPTIRIM; breeding; cattle; parentage;
XX	KM	genetic mapping; traits; amplification; ss.
XX	OS	Bos taurus.
XX	PN	MO9213102-A1.
XX	PD	06-AUG-1992.
XX	PF	15-JAN-1992; 92WO-US000340.
XX	PR	15-JAN-1991; 91US-00642342.
XX	PA	(GENM-) GENMARK.
XX	PI	Georges M, Massey JM;
XX	DR	WPI; 1992-284684/34.
XX	PT	Polymorphic bovine DNA markers - used in genetic identification, gene
XX	PS	mapping, and selective breeding.
XX	PS	Table 7; Page 357; 517pp; English.
CC	CC	The sequence is that of a bovine microsatellite sequence obtd. by
CC	CC	screening a library of bovine MbOI DNA fragments of between 250 and 500
CC	CC	bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC	CC	clones cross-hybridised. Assuming independent distribution of
CC	CC	microsatellites and MbOI sites, the frequency of (76)n >9 microsatellites
CC	CC	in the bovine genome is estimated at >100,000. The sequence information
CC	CC	for ca. 230 such bovine microsatellites is summarised in the
CC	CC	specification and indexed herein (see below). The sequences upstream and
CC	CC	downstream of the microsatellite sequence were used to generate the
CC	CC	required PCR primers for in vitro amplification of the corresp.
CC	CC	microsatellite (using the program OPTIRIM). The microsatellites may be
CC	CC	used to identify individuals, for percentage testing, and in the genetic
CC	CC	mapping of economic trait loci, or genes involved the determination of
CC	CC	economically important traits esp. in cattle, to allow selective
CC	CC	breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
SO	XX	field.)
SO	XX	Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
Query Match	0.4%; Score 24; DB 1; Length 24;	
Best Local Similarity	100.0%; Pired. No. 22;	
Matches 24; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
OY	4996 GTGTGTTGTGTGTGTGTGTGTGTGT 5019	
DB		
1	GTGTGTGTGTGTGTGTGTGTGTGTGT 24	
RESULT 38		
AAQ34024		
ID	AAQ34024 standard; DNA; 24 BP.	
XX	AAQ34024;	
XX	AC	
XX	DT	25-MAR-2003 (revised)
XX	DT	02-FEB-1993 (first entry)
DE	XX	Microsatellite sequence from clone TGLA423.
XX	XX	
KM	PCF; selection; primers; OPTIRIM; breeding; cattle; parentage;	
KM	genetic mapping; traits; amplification; ss.	
XX	XX	
OS	Bos taurus.	
XX	XX	
PN	MO9213102-A1.	
XX	XX	
PD	06-AUG-1992.	

```

XX PF 15-JAN-1992; 92WO-US000340.
XX PT mapping, and selective breeding.
XX PR 15-JAN-1991; 91US-00642342.
XX PS (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PS Table 7, Page 340; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obtd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100, 000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX CC specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX CC required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program OPTIPRIM). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX CC mapping of economic trait loci, or genes involved the determinism of
XX economically important traits esp. in cattle, to allow selective
XX CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
Query Match 0.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4997 TGTGTGTGTGTGTGTGTGTGTGTG 5020
DB 1 TGTGTGTGTGTGTGTGTGTGTGTG 24
RESULT 39
AAQ33707
ID AAQ33707 standard; DNA; 24 BP.
XX AC AAQ33707;
XX DT 25-MAR-2003 (revised)
XX DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA131.
XX KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
XX genetic mapping; traits; amplification; ss.
XX OS Bos taurus.
XX PN MO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PS (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.

```

```

XX PS Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PR 15-JAN-1991; 91US-00642342.
XX PS Table 7, Page 213; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obtd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100, 000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX CC specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX CC required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program OPTIPRIM). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX CC mapping of economic trait loci, or genes involved the determinism of
XX economically important traits esp. in cattle, to allow selective
XX CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
Query Match 0.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4997 TGTGTGTGTGTGTGTGTGTGTGTG 5020
DB 1 TGTGTGTGTGTGTGTGTGTGTGTG 24
RESULT 40
AAT66096/c
ID AAT66096 standard; DNA; 24 BP.
XX AC AAT66096;
XX DT 25-MAR-2003 (revised)
XX DT 18-JUN-1997 (first entry)
XX DE Repeat sequence found in the human chromosomal clone UW42.
XX KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
XX PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
XX linkage analysis; genetic disease; animal; plant; breeding; locus;
XX hybridisation; chromosome; ds.
XX OS Homo sapiens.
XX PN US5582979-A.
XX PD 10-DEC-1996.
XX PF 04-APR-1994; 94US-00222177.
XX PR 21-APR-1989; 89US-00341562.
XX PR 05-SEP-1991; 91US-00754351.
XX PS (MARS-) MARSHFIELD CLINIC.
XX PI Weber JL;
XX DR WPI; 1997-042299/04.
XX PT Detection of polymorphic genetic markers of the form (dc-dA)n(dc-dT)n -
XX using novel nucleic acid mols. as primers.
XX PS Example 9; Col 61-62; 186pp; English.
XX CC The invention relates to the isolation of polymorphic repeat sequences

```

```
CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
CC and hormone dependence
XX
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
Query Match 0.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

1. ☐ **Very poor**
 2. ☐ **Poor**
 3. ☐ **Fair**
 4. ☐ **Good**
 5. ☐ **Very good**
 6. ☐ **Excellent**
 7. ☐ **Outstanding**
 8. ☐ **Superb**
 9. ☐ **Amazing**
 10. ☐ **Unbelievable**
 11. ☐ **Incredible**
 12. ☐ **Unfathomable**
 13. ☐ **Unimaginable**
 14. ☐ **Unconceivable**
 15. ☐ **Unfathomable**
 16. ☐ **Unimaginable**
 17. ☐ **Unconceivable**
 18. ☐ **Unfathomable**
 19. ☐ **Unimaginable**
 20. ☐ **Unconceivable**
 21. ☐ **Unfathomable**
 22. ☐ **Unimaginable**
 23. ☐ **Unconceivable**
 24. ☐ **Unfathomable**
 25. ☐ **Unimaginable**
 26. ☐ **Unconceivable**
 27. ☐ **Unfathomable**
 28. ☐ **Unimaginable**
 29. ☐ **Unconceivable**
 30. ☐ **Unfathomable**
 31. ☐ **Unimaginable**
 32. ☐ **Unconceivable**
 33. ☐ **Unfathomable**
 34. ☐ **Unimaginable**
 35. ☐ **Unconceivable**
 36. ☐ **Unfathomable**
 37. ☐ **Unimaginable**
 38. ☐ **Unconceivable**
 39. ☐ **Unfathomable**
 40. ☐ **Unimaginable**
 41. ☐ **Unconceivable**
 42. ☐ **Unfathomable**
 43. ☐ **Unimaginable**
 44. ☐ **Unconceivable**
 45. ☐ **Unfathomable**
 46. ☐ **Unimaginable**
 47. ☐ **Unconceivable**
 48. ☐ **Unfathomable**
 49. ☐ **Unimaginable**
 50. ☐ **Unconceivable**
 51. ☐ **Unfathomable**
 52. ☐ **Unimaginable**
 53. ☐ **Unconceivable**
 54. ☐ **Unfathomable**
 55. ☐ **Unimaginable**
 56. ☐ **Unconceivable**
 57. ☐ **Unfathomable**
 58. ☐ **Unimaginable**
 59. ☐ **Unconceivable**
 60. ☐ **Unfathomable**
 61. ☐ **Unimaginable**
 62. ☐ **Unconceivable**
 63. ☐ **Unfathomable**
 64. ☐ **Unimaginable**
 65. ☐ **Unconceivable**
 66. ☐ **Unfathomable**
 67. ☐ **Unimaginable**
 68. ☐ **Unconceivable**
 69. ☐ **Unfathomable**
 70. ☐ **Unimaginable**
 71. ☐ **Unconceivable**
 72. ☐ **Unfathomable**
 73. ☐ **Unimaginable**
 74. ☐ **Unconceivable**
 75. ☐ **Unfathomable**
 76. ☐ **Unimaginable**
 77. ☐ **Unconceivable**
 78. ☐ **Unfathomable**
 79. ☐ **Unimaginable**
 80. ☐ **Unconceivable**
 81. ☐ **Unfathomable**
 82. ☐ **Unimaginable**
 83. ☐ **Unconceivable**
 84. ☐ **Unfathomable**
 85. ☐ **Unimaginable**
 86. ☐ **Unconceivable**
 87. ☐ **Unfathomable**
 88. ☐ **Unimaginable**
 89. ☐ **Unconceivable**
 90. ☐ **Unfathomable**
 91. ☐ **Unimaginable**
 92. ☐ **Unconceivable**
 93. ☐ **Unfathomable**
 94. ☐ **Unimaginable**
 95. ☐ **Unconceivable**
 96. ☐ **Unfathomable**
 97. ☐ **Unimaginable**
 98. ☐ **Unconceivable**
 99. ☐ **Unfathomable**
 100. ☐ **Unimaginable**
 101. ☐ **Unconceivable**
 102. ☐ **Unfathomable**
 103. ☐ **Unimaginable**
 104. ☐ **Unconceivable**
 105. ☐ **Unfathomable**
 106. ☐ **Unimaginable**
 107. ☐ **Unconceivable**
 108. ☐ **Unfathomable**
 109. ☐ **Unimaginable**
 110. ☐ **Unconceivable**
 111. ☐ **Unfathomable**
 112. ☐ **Unimaginable**
 113. ☐ **Unconceivable**
 114. ☐ **Unfathomable**
 115. ☐ **Unimaginable**
 116. ☐ **Unconceivable**
 117. ☐ **Unfathomable**
 118. ☐ **Unimaginable**
 119. ☐ **Unconceivable**
 120. ☐ **Unfathomable**
 121. ☐ **Unimaginable**
 122. ☐ **Unconceivable**
 123. ☐ **Unfathomable**
 124. ☐ **Unimaginable**
 125. ☐ **Unconceivable**
 126. ☐ **Unfathomable**
 127. ☐ **Unimaginable**
 128. ☐ **Unconceivable**
 129. ☐ **Unfathomable**
 130. ☐ **Unimaginable**
 131. ☐ **Unconceivable**
 132. ☐ **Unfathomable**
 133. ☐ **Unimaginable**
 134. ☐ **Unconceivable**
 135. ☐ **Unfathomable**
 136. ☐ **Unimaginable**
 137. ☐ **Unconceivable**
 138. ☐ **Unfathomable**
 139. ☐ **Unimaginable**
 140. ☐ **Unconceivable**
 141. ☐ **Unfathomable**
 142. ☐ **Unimaginable**
 143. ☐ **Unconceivable**
 144. ☐ **Unfathomable**
 145. ☐ **Unimaginable**
 146. ☐ **Unconceivable**
 147. ☐ **Unfathomable**
 148. ☐ **Unimaginable**
 149. ☐ **Unconceivable**
 150. ☐ **Unfathomable**
 151. ☐ **Unimaginable**
 152. ☐ **Unconceivable**
 153. ☐ **Unfathomable**
 154. ☐ **Unimaginable**
 155. ☐ **Unconceivable**
 156. ☐ **Unfathomable**
 157. ☐ **Unimaginable**
 158. ☐ **Unconceivable**
 159. ☐ **Unfathomable**
 160. ☐ **Unimaginable**
 161. ☐ **Unconceivable**
 162. ☐ **Unfathomable**
 163. ☐ **Unimaginable**
 164. ☐ **Unconceivable**
 165. ☐ **Unfathomable**
 166. ☐ **Unimaginable**
 167. ☐ **Unconceivable**
 168. ☐ **Unfathomable**
 169. ☐ **Unimaginable**
 170. ☐ **Unconceivable**
 171. ☐ **Unfathomable**
 172.

RESULT 42

ID	AAH46016 standard; DNA; 24 BP.
XX	
AC	AAH46016;

XX
DE
XX

Synthetic oligonucleotide 16.

Lymphoma;

OS Synthetic.

PN	WO200144465-A2.
XX	
XX	
PD	21-JUN-2001.
XX	

XX

PR 29-AUG-2000; 2000US-0228925P.

PA (BION-) BIONICHE LIFE SCI INC.

Phillips NC, Fillion

DR WPI; 2001-398150/42.

Composition comprising synthetic

PT inducing cell cycle arrest

XX
XX
01318 61 Page 17, English

The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific

are useful for inducing cell cycle

Query Match	Score	DB	Length
Best Local Similarity	100.0%	Pred. No. 22;	
cytokine such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/CIP, p15(Ink4B), p16(Ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone dependence	0.4%;	24;	24;
Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;			
xx			
xx			

RESULT 44

01 24-APR-2003 (LIST ENCLY)
XX

DE Human RNA polymerase I-40 kDa subunit 9.68 PCR primer #1.
 XX
 XX Human; RNA polymerase I-40 kDa subunit 9.68; cancer; cytostatic;
 KW HIV infection; anti-HIV; PCR; primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX CN1363655-A.
 PN
 XX
 XX 14-AUG-2002.
 PD
 XX 05-JAN-2001; 2001CN-00105029.
 PF
 XX 05-JAN-2001; 2001CN-00105029.
 PR
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA
 XX Mao Y, Xie Y;
 PI
 XX WPI; 2002-742064/81.
 DR
 XX
 XX Polypeptide-human RNA polymerase I-40 kDa subunit 9.68 and polynucleotide
 PT for coding it.
 PS
 XX Example 2; Page 17 (Disclosure); 32pp; Chinese.
 XX
 XX The present invention relates to human RNA polymerase I-40 kDa subunit
 CC 9.68 (see ABP59130). The protein can be used for treating diseases such
 CC as cancer and HIV infection. The present sequence is a PCR primer, which
 CC was used in an example from the invention
 CC
 XX Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1469 GAACCTGCTGACCTCAGTGATCCA 1492
 DB 1 GAACCTGCTGACCTCAGTGATCCA 24

RESULT 46
 ACH03377
 ID ACH03377 standard; DNA; 24 BP.
 AC ACH03377;
 XX
 DT 25-SEP-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #1012.
 XX
 XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 XX
 OS Synthetic.
 XX
 XX US2003050268-A1.
 PN
 XX 13-MAR-2003.
 PD
 XX 29-MAR-2002; 2002US-00112653.
 PF
 XX 29-MAR-2001; 2001US-0279642P.
 PR
 XX (KRIE/) KRIEG A M.
 PA (BERG/) BERG D J.
 XX
 XX Krieg AM, Berg DJ;
 PI
 XX WPI; 2003-521815/49.
 DR

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.
 XX
 XX Disclosure; Page 36; 229pp; English.
 PS
 XX The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid
 CC
 XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGTG 5020
 DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTG 24

RESULT 47
 ADB37364
 ID ADB37364 standard; DNA; 24 BP.
 AC ADB37364;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #978.
 XX
 XX de; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX
 OS Synthetic.
 XX
 XX US2003087848-A1.
 PN
 XX 08-MAY-2003.
 PD
 XX 02-FEB-2001; 2001US-00776479.
 PF
 XX 03-FEB-2000; 2000US-0179991P.
 PR
 XX (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 XX (FOUR/) FOURON Y.
 PI Bratzler RL, Petersen DM, Fouron Y;
 XX
 XX WPI; 2003-657977/62.
 DR
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 PT
 XX Disclosure; Page 20; 221pp; English.
 PS
 XX The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 CC
 XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 24; DB 1; Length 24;

KM	genetic mapping; traits; amplification; ss.
XX	
OS	Bos taurus.
XX	
PN	WO9213102-A1.
XX	
PD	06-AUG-1992.
XX	
PF	15-JAN-1992; 92MO-US000340.
XX	
PR	15-JAN-1991; 91US-00642342.
XX	
PA	(GENM-) GENMARK.
PI	Georges M, Massey JM;
PI	WPI; 1992-284684/34.
DR	
XX	
PT	Polymorphic bovine DNA markers - used in genetic identification, gene
XX	mapping, and selective breeding.
PS	Table 7; Page 263; 517pp; English.
XX	
CC	The sequence is that of a bovine microsatellite sequence obtd. by
CC	screening a library of bovine Mbol DNA fragments of between 250 and 500
CC	bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC	clones cross-hybridised. Assuming independent distribution of
CC	microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
CC	in the bovine genome is estimated at >100, 000. The sequence information
CC	for ca. 230 such bovine microsatellites is summarised in the
CC	specification and indexed herein (see below). The sequences upstream and
CC	downstream of the microsatellite sequence were used to generate the
CC	required PCR primers for in vitro amplification of the corresp.
CC	microsatellite (using the program OPrIPRM). The microsatellites may be
CC	used to identify individuals, for parentage testing, and in the genetic
CC	mapping of economic trait loci or genes involved in the determination of
CC	economically important traits esp. in cattle, to allow selective
CC	breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC	field.)
XX	
SO	Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
XX	
Query Match	0.4%; Score 23; DB 1; Length 23;
Best Local Similarity	100.0%; Fred.No.26;
Matches 23; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	4997 TGCTGTGCTGTGCTGTGCTGTGCT 5019 1 TGCTGTGCTGTGCTGTGCTGTGCT 23
Db	
RESULT 51	
AAT6105/c	
ID	AAT66105 standard; DNA; 23 BP.
XX	
AC	AAT66105;
XX	
DT	25-MAR-2003 (revised)
DT	18-JUN-1997 (first entry)
DE	Repeat sequence found in the human chromosomal clone SW13.
XX	
KM	Polymorphism; repeat sequence; genetic marker; primer; amplification;
KM	PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KM	linkage analysis; genetic disease; animal; plant; breeding; locus;
KM	hybridisation; chromosome; ds.
XX	
OS	Homo sapiens.
XX	
PN	U55582979-A.
XX	
PD	10-DEC-1996.
XX	

```
PF      04-APR-1994;    94US-00222177.
XX
XX      21-APR-1989;    89US-00341562.
PR      05-SEP-1991;    91US-00754351.
XX
XX      (MARS-) MARSHFIELD CLINIC.
PA
XX      Weber JL;
PI
XX      WPI; 1997-042299/04.
XX
XX      Detection of polymorphic genetic markers of the form (dC-dA)n(dC-dT)n -
PT      using novel nucleic acid mols. as primers.
XX
XX      Example 9; Col 61-62; 186pp; English.
XX
CC      The invention relates to the isolation of polymorphic repeat sequences
CC      having the sequence (dC-dA)n.(dC-dT)n which can be used as genetic
CC      markers. Primers based on these sequences can be used to detect these
CC      repeats, especially for use in e.g paternity or maternity testing, human
CC      genetic analysis such as linkage analysis of genetic disease, commercial
CC      animal or plant breeding or pedigree analysis. The sequences AAT66084-
CC      T66107 represent repeat sequences of low informativeness found in
CC      specific human genes. This repeat sequence is found in the human
CC      chromosomal clone SW13. The sequence is amplified by primers AAT66106-7.
CC      (updated on 25-MAR-2003 to correct PF field.)
XX
SQ      Sequence 23 BP; 12 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
        Query Match          0.4%; Score 23; DB 1; Length 23;
        Best Local Similarity 100.0%; Pred. No. 26;
        Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4997 TGGTGTTGGTGTTGGTGTTGGTGT 5019
DB      23 TGTGTGTGTGTGTGTGTGTGTGTGT 1
RESULT 52
AAF60472/c
ID      AAF60472 standard; DNA; 23 BP.
XX
XX      AAF60472;
AC
DT      27-APR-2001 (first entry)
XX
DE      Oligonucleotide clamp #17.
XX
KM      Oligonucleotide clamp; ds.
XX
OS      Unidentified.
XX
FN      US6180777-B1.
PD      30-JAN-2001.
PF      03-JAN-1997;    97US-00787321.
PR      12-JAN-1996;    96US-0009918P.
PA      (FARB ) BAYER CORP.
XX      Horn T;
PI
XX      WPI; 2001-201911/20.
XX
XX      Synthesizing branched nucleic acids useful as diagnostic and molecular
XX      probes, involves combining first units having haloalkylamino groups and
XX      second units having thiol or phosphorothioate groups.
XX
XX      Example 7; Col 19; 20pp; English.
XX
XX      The present invention relates to a method for synthesising a branched or
```

[illegible]

RESULT 55
AAQ3675
ID AAQ3675 standard; DNA; 22 BP.
XX
XX AAQ3675;
AC
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA117.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KM genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
OS
XX
XX W09213102-A1.
XX
XX PD 06-AUG-1992.
XX
XX PF 15-JAN-1992; 92WO-US000340.
XX
XX PR 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX
XX WPI; 1992-284684/34.
XX
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX
XX Table 7; Page 199; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;

Query Match 0.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTG 5018
DB 1 TGTGTGTGTGTGTGTGTGTGTG 22

RESULT 56
AAQ34038
ID AAQ34038 standard; DNA; 22 BP.
XX
XX AAQ34038;
AC
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)

XX
XX Microsatellite sequence from clone TGLA432.
DE
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KM genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
OS
XX
XX W09213102-A1.
XX
XX PD 06-AUG-1992.
XX
XX PF 15-JAN-1992; 92WO-US000340.
XX
XX PR 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX
XX WPI; 1992-284684/34.
XX
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX
XX Table 7; Page 346; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;

Query Match 0.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTG 5018
DB 1 TGTGTGTGTGTGTGTGTGTGTG 22

RESULT 57
AAQ34080
ID AAQ34080 standard; DNA; 22 BP.
XX
XX AAQ34080;
AC
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)

DE Microsatellite sequence from clone TGLA48.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KM genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
OS
XX
XX W09213102-A1.

XX	WP1; 1992-284684/34.
XX	PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX	FT mapping, and selective breeding.
PS	Table 7; Page 327; 517p; English.
XX	The sequence is that of a bovine microsatellite sequence obt'd. by
CC	screening a library of bovine MboI DNA fragments of between 250 and 500
CC	bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC	clones cross-hybridised. Assuming independent distribution of
CC	microsatellites and MboI sites, the frequency of (T6/n >9 microsatellites
CC	in the bovine genome is estimated at >100, 000. The sequence information
CC	for ca. 230 such bovine microsatellites is summarised in the
CC	specification and indexed herein (see below). The sequences upstream and
CC	downstream of the microsatellite sequence were used to generate the
CC	required PCR primers for in vitro amplification of the corresp.
CC	microsatellite (using the program OPTPRIM). The microsatellites may be
CC	used to identify individuals, for parentage testing, and in the genetic
CC	mapping of economic trait loci, or genes involved the determination of
CC	economically important traits esp. in cattle, to allow selective
CC	breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC	field.)
SQ	Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
Query Match	0.4%; Score 22; DB 1; Length 22;
Best Local Similarity	100.0%; Pred.No. 29;
Matches 22; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	4997 TGTGTTGTGTTGTGTTGTGTTGTG 5018 1 TGTGTTGTGTTGTGTTGTGTTGTG 22
ID	AAQ83952/c
XX	AAQ83952 standard; DNA; 22 BP.
AC	AAQ83952;
XX	25-MAR-2003 (revised)
DT	04-OCT-1995 (first entry)
DE	Oligonucleotide clamp n, for producing comb-type branched polymer.
XX	HIV; pol; nef, oligonucleotide clamp; branched; macromolecule; ss.
OS	Synthetic.
XX	key
FT	modified_base
FT	location/Qualifiers
FT	1
FT	/*tag= a
FT	/note= "Modified with BrrCH2(=O)CNR-"
FT	8..9
FT	/*tag= b
FT	/note= "C(pnp)/A, pnp = a linkage or monomer containing a
FT	bromacetyl amino functionality, and p = phosphodiester
FT	linkage"
FT	14..15
FT	/*tag= c
FT	/note= "C(pnp)/A, pnp = a linkage or monomer containing a
FT	bromacetyl amino functionality, and p = phosphodiester
FT	linkage"
FT	21..22
FT	/*tag= d
FT	/note= "C(pnp)/A, pnp = a linkage or monomer containing a
FT	bromacetyl amino functionality, and p = phosphodiester
FT	linkage"
XX	MO9501365-A1.
XN	12-JAN-1995.
XD	

Thu Sep 23 10:01:06 2004

schul tz881-3.rng

Page 27

[illegible][illegible]

[illegible]

KM	Immune system mediated disease; gamma-interferon; IL-8; ss.
OS	Synthetic.
PN	US5932556-A.
XX	
PD	03-AUG-1999.
XX	
PF	18-SEP-1995; 95US-00529878.
XX	
PR	09-FEB-1995; 95US-00387041.
FR	18-SEP-1995; 95US-00529878.
XX	
PA	(TAMR/) TAM R C.
XX	
PI	Tam RC;
XX	
DR	WPI; 1996-384228/38.
XX	
PT	Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
PT	
XX	
PS	Example; Col 13; 45pp; English.
XX	
CC	The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises administering to a subject in need thereof an oligonucleotide (OGN). AAX9028 to CC AAX90291 represent specificationally claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. CC AAX90292 to AAX90323 represent oligonucleotides used in the exemplification of the present invention
CC	
XX	
SQ	Sequence 21 BP; 0 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
XX	
Query Match	0.3%; Score 21; DB 1; Length 21;
Best Local Similarity	100.0%; Pred.No. 34;
Matches 21; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
CY	4996 GTGTGTTGTGTGTGTGTGTGTGTG 5016 1 GTGTGTTGTGTGTGTGTGTGTGTG 21
DB	
RESULT 66	
AAT65738/C	
ID	AAT65738 standard; DNA; 21 BP.
XX	
AC	AAT65738;
XX	
DT	25-MAR-2003 (revised)
DT	17-JUN-1997 (first entry)
DE	Repeat sequence from polymorphic marker clone Mf437.
XX	
KW	Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
XX	
OS	Homo sapiens.
XX	
PN	US5582979-A.
XX	
PD	10-DEC-1996.
XX	
PF	04-APR-1994; 94US-00222177.
XX	
PR	21-APR-1989; 89US-00341562.
PR	05-SEP-1991; 91US-00754351.
XX	
PA	(MARSH-) MARSHFIELD CLINIC.
XX	

PI	Weber JL,
XX	
DR	WPI; 1997-042239/04.
PT	Detection of polymorphic genetic markers of the form (dc-da)n(dg-dt)n -
XX	using novel nucleic acid mois. as primers.
PS	Disclosure; Col 9-10; 186pp; English.
CC	The invention relates to the isolation of polymorphic repeat sequences
CC	having the sequence (dc-da)n.(dg-dt)n which can be used as genetic
CC	markers. Primers based on these sequences can be used to detect these
CC	repeats, especially for use in e.g paternity or maternity testing, human
CC	genetic analysis such as linkage analysis of genetic disease, commercial
CC	animal or plant breeding or pedigree analysis. Clones containing the
CC	repeat sequences were isolated by hybridisation of chromosome-specific
CC	phage libraries with a synthetic poly(dc-da).(dg-dt) probe. Over 100
CC	repeat blocks were isolated. The inserts from the clones were amplified
CC	by primers AAT55798-166047. Those clones where the repeat sequence has
CC	been determined are shown in AAT55704-797. This repeat sequence is from
CC	the marker clone Md537 which contains the repeat sequence having the
CC	formula: (Ac)10A. (Updated on 25-MAR-2003 to correct PF field.)
XX	
SQ	Sequence 21 BP; 11 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
Query Match	0.3%; Score 21; DB 1; Length 21;
Best Local Similarity	100.0%; Pred.No. 34;
Matches 21; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Oy	4997 TGTCGTGCTGCTGCTGCTGCT 5017
Db	21 TGTGTGTGTGTGTGTGTGTGT 1
RESULT 67	
AAV51377/c	
ID	AAV51377 standard; DNA; 21 BP.
AC	AAV51377;
XX	
DT	27-OCT-1998 (first entry)
XX	
DE	Human TIGR PCR primer Pr-2(4A).
KW	TIGR, trabecular meshwork induced glucocorticoid response protein; human;
KW	diagnosis; glaucoma; polymorphism; steroid sensitivity; PCR primer; ss.
OS	Synthetic.
OS	Homo sapiens.
PN	M09832850-A1.
PD	30-JUL-1998.
PF	09-JAN-1998; 98WO-US0000468.
PR	28-JAN-1997; 97US-00791154.
PR	26-SEP-1997; 97US-00938669.
PA	(REGC) UNITV CALIFORNIA.
PI	Nguyen TD, Polansky JR, Chen P, Chen H;
XX	
DR	WPI; 1998-427946/36.
PT	Use of TIGR nucleic acid sequences - used for, e.g. developing products
PT	for diagnosis, prognosis and treatment of glaucoma.
PS	Claim 9; Page 9; 105pp; English.
CC	AAV51371-VS1390 are PCR primers used in the amplification of a novel
CC	human trabecular meshwork induced glucocorticoid response protein (TIGR)
CC	promoter region which is used in a method for diagnosing glaucoma in a

```
CC patient The method involves the detection of polymorphisms whose
CC presence is predictive of a mutation affecting TIGR response in the
CC patient and can be diagnostic of glaucoma or steroid sensitivity. Base
CC substitutions and base additions upstream of and within TIGR exons can
CC also be used to diagnose glaucoma
XX
SQ Sequence 21 BP; 8 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
OY Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 34;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB 4394 CAGTTGTCACATACGTGT 4414
21 CAGTGTGCAGATACGTGT 1
RESULT 68
AAVS1373/C
ID AAVS1373 standard; DNA; 21 BP.
AC AAVS1373;
XX 27-OCT-1998 (first entry)
DT Human TIGR PCR primer CA2.
DE
XX TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KM diagnosis; glaucoma; polymorphism; steroid sensitivity; PCR primer; ss.
XX OS Synthetic.
OS Homo sapiens.
XX MO9832850-AI.
PN 30-JUL-1998.
PD
XX 09-JAN-1998; 98MO-US000468.
PF 28-JAN-1997; 97US-00791154.
PR 26-SEP-1997; 97US-00938669.
XX (REGC ) UNTV CALIFORNIA.
PA Nguyen TD, Polansky JR, Chen P, Chen H;
PI WPI; 1998-427946/36.
XX
XX Use of TIGR nucleic acid sequences - used for, e.g. developing products
PT for diagnosis, prognosis and treatment of glaucoma.
XX Claim 9; Page 9; 105pp; English.
PS
XX AAVS1371-VS1390 are PCR primers used in the amplification of a novel
XX human trabecular meshwork induced glucocorticoid response protein (TIGR)
XX promoter region which is used in a method for diagnosing glaucoma in a
XX patient. The method involves the detection of polymorphisms whose
XX presence is predictive of a mutation affecting TIGR response in the
XX CC patient and can be diagnostic of glaucoma or steroid sensitivity. Base
XX substitutions and base additions upstream of and within TIGR exons can
XX also be used to diagnose glaucoma
CC
SQ Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
OY Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 34;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0,
DB 5047 CTATTATTGGGGTATGGGTGC 5067
21 CTATTATTGGGGTATGGGTGC 1
```

RESULT 69

AA57495/C

ID AA57495 standard; DNA; 21 BP.

XX AA57495;

DT 20-OCT-2000 (first entry)

XX Primer used for SSCP screening of the human TIGR gene.

XX TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;

XX glaucoma; steroid sensitivity; progressive ocular hypertension;

XX vision loss; primer; ss.

XX Homo sapiens.

XX WO200042220-A1.

XX 20-JUL-2000.

XX 11-JAN-2000; 2000WO-US000559.

XX 11-JAN-1999; 99US-00227881.

XX 07-MAY-1999; 99US-00306828.

XX (REGC) UNIV CALIFORNIA.

XX Nguyen TD, Polansky JR, Chen P, Chen H;

XX WPI, 2000-491060/43.

XX diagnosis, prognosis and treatment of glaucoma, based on detecting

XX specific polymorphisms in the promoter of the trabecular meshwork

XX inducible glucocorticoid receptor gene.

XX Claim 9; Page 53; 122pp; English.

XX Primers AA57489-A57508 were used for single strand conformational

XX polymorphism (SSCP) screening of the human TIGR (trabecular meshwork

XX inducible glucocorticoid receptor) gene. The primers correspond to

XX sequences found within the TIGR promoter and two of the exons of TIGR,

XX and are used in the method of the invention. The specification describes

XX a method for the diagnosis, prognosis and treatment of glaucoma, based on

XX detecting specific polymorphisms in the promoter of the TIGR gene. The

XX method is used for diagnosis and prognosis of glaucoma (of all types),

XX steroid sensitivity and progressive ocular hypertension that leads to

XX loss of vision. Glaucoma can be treated by administering an agent that

XX binds to cis-acting elements within the TIGR promoter. The TIGR promoter

XX (or other regulatory regions) can be used to express homologous or

XX heterologous genes, particularly for tissue-specific expression of

XX therapeutic transgenes for treating glaucoma, also to generate transgenic

XX animals and in screening for compounds (specific modulators) with

XX diagnostic or therapeutic potential. Fragments of the TIGR sequence can

XX be used as amplification primers or probes, e.g. for isolating related

XX sequences in non-human animals

XX Sequence 21 BP; 8 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

XX Query Match 0.3%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 34;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX DB 4394 CAGTTGTGAGATACCTTGT 4414

XX 21 CAGTTGTGAGATACCTTGT 1

XX RESULT 70

XX AA57491/C

XX ID AA57491 standard; DNA; 21 BP.

XX AA57491;

XX RESULT 71

XX AAH46013

XX ID AAH46013 standard; DNA; 21 BP.

XX AAH46013;

XX DT 12-SEP-2001 (first entry)

XX Synthetic oligonucleotide 13.

XX Synthetic oligonucleotide repeat; cytosinatic; apoptosis;

XX cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;

XX Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

XX Query Match 0.3%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 34;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX DB 5047 CTATTATGGGATGGTGC 5067

XX 21 CTATTATGGGATGGTGC 1

PD	XX	21-JUN-2001.
PF	XX	12-DEC-2000; 2000MO-CA001467.
PR	XX	13-DEC-1999; 99US-0170325P.
PR	XX	29-AUG-2000; 2000US-0228925P.
PA	XX	(BION-) BIONICHE LIFE SCI INC.
PT	XX	Phillips NC, Filion MC;
DR	XX	WP1; 2001-398150/42.
PT	XX	Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating caspases.
PT	XX	Example 4; Page 17; 77p; English.
CC	XX	The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (Il)-1-beta, Il-6, Il-10, Il-12 and tumour necrosis factor (TNF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/Cip, p15(Ink4B), p16(Ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone dependence
SQ	XX	Sequence 21 BP; 0 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
QY	DB	Query Match Best Local Similarity 100.0%; Score 21; DB 1; Length 21; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB	QY	4996 GGCTGGCTGCTGGCTGGCTG 5016 1 GGCTGGCTGCTGGCTGGCTG 21
ID	AAFP9702	AAFP9702 standard; DNA; 21 BP.
AC	AAFP9702;	
DT	12-JUN-2001	(first entry)
DE	Immunostimulatory nucleic acid #818.	
KW	Vaccine; cytostatic; vituocidal; bacteriocidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.	
OS	Synthetic.	
PN	WO200122972-A2.	
PD	05-APR-2001.	
PE	25-SEP-2000; 2000MO-US026383.	
PR	25-SEP-1999; 99US-0156113P.	
PR	27-SEP-1999; 99US-0156135P.	
PR	23-AUG-2000; 2000US-0227436P.	

XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
XX Claim 2; Page 35; 276dp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rheobiosis, Oeler-Weber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasis, haemophillic joints, angiodiroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention

SO Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Fred. No. 34;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4997 TGTGTTGTGTGTGTGTGTGTGT 5017
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 21

RESULT 75
ACF64053
ID ACF64053 standard; DNA; 21 BP.
XX ACF64053;
AC ACF64053;
DT 13-OCT-2003 (first entry)
XX
DE IFNARI forward PCR primer #29.
XX
KW Human; detection; computer-readable storage medium; polymorphic site;
KM signal carrying data; data processing system; multiple sclerosis;
KN PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003014319-A2.
XX
PD 20-FEB-2003.
XX
PF 07-AUG-2002; 2002WO-US025268.
XX
PR 07-AUG-2001; 2001US-0310741P.
PR 24-SEP-2001; 2001US-0324790P.
FA (DNAS-) DNA SCT INC.
FI Jones HB, Xu H, White R, Rienhoff HY, Jin W, Natsoulis G;
PI WPI; 2003-268196/26.
XX
DR New polynucleotide, useful for detecting loci associated with multiple
PT sclerosis.
XX
PS Disclosure; Page 10; 93pp; English.
XX
CC The present invention describes an isolated polynucleotide (PN)
CC comprising: (a) a sequence comprising at least five contiguous nucleotides
CC of a sequence comprising variant sequences (A) from Table 4 given in the
CC specification; or (b) a sequence that is complementary to (a). Also

described: (1) an array of (PN)s comprising two or more of the isolated (PN)s; (2) detecting a (PN) in an individual; (3) a computer-readable storage medium, where each record has a field identifying a base occupying a (PN) site and a location of the polymorphic site; and (4) a signal carrying data for access by an application program having executed on a data processing system. The (PN) can be used for detecting loci associated with multiple sclerosis. ACP64025 to ACP64424 represent sequences used in the exemplification of the present invention

Sequence 21 BP; 4 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 34; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1471 ACTCCTGACCTGAGTGATCC 1491

DB 1 ACTCCTGACCTGAGTGATCC 21

RESULT 76

ID ACH03241 standard; DNA; 21 BP.

AC ACH03241;

DT 25-SEP-2003 (first entry)

DE Immunostimulatory nucleic acid #876.

KW Immunostimulatory; anti-inflammatory; dermatological; antipsoriatic;

KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;

KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

OS Synthetic.

PN US2003050268-A1.

PD 13-MAR-2003.

PF 29-MAR-2002; 2002US-00112653.

PR 29-MAR-2001; 2001US-0279642P.

PA (KRIE/) KRIEG A M.

PA (BERG/) BERG D U.

PI Krieg AM, Berg DJ;

PT WPI; 2003-521815/49.

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,

PT allergic contact dermatitis, latex dermatitis or inflammatory bowel

PT disease by administering an immunostimulatory nucleic acid.

PS Disclosure; Page 32; 229pp; English.

CC The invention describes a method of treating non-allergic inflammatory

CC disease comprising administering to a subject having or at risk of

CC developing a non-allergic inflammatory disease an immunostimulatory

CC nucleic acid for prevention or treatment of the disease. The method is

CC useful for treating non-allergic inflammatory diseases, such as

CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or

CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.

CC This sequence represents an immunostimulatory nucleic acid

CC Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;

QY 4997 TGTGTGTGTGTGTGTGTGTGT 5017

DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 77

ID ADB37204 standard; DNA; 21 BP.

AC ADB37204;

DT 04-DEC-2003 (first entry)

DE Immunostimulatory nucleic acid #818.

KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;

KW hypo-responsive subject; immunostimulatory.

OS Synthetic.

PN US2003087848-A1.

PD 08-MAY-2003.

PF 02-FEB-2001; 2001US-00776479.

PR 03-FEB-2000; 2000US-0179991P.

PA (BRAT/) BRATZLER R L.

PA (PETE/) PETERSEN D M.

PA (FOUR/) FOURON Y.

PI Bratzler RL, Petersen DM, Fouron Y;

PT WPI; 2003-657977/62.

PT Treating and/or preventing allergy or asthma using an immunostimulatory

PT nucleic acid alone or in combination with an asthma/allergy medicament.

PS Disclosure; Page 17; 221pp; English.

CC The invention relates to a method of treating or preventing allergy or

CC asthma which comprises administering to a subject a poly-G nucleic acid

CC in an aerosol formulation. The methods and compositions of the present

CC invention are useful for diagnosing and/or treating asthma and allergy

CC especially in a hypo-responsive subject. The present sequence represents

CC an immunostimulatory nucleic acid of the invention.

CC Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGT 5017

DB 1 TGTGTGTGTGTGTGTGTGTGT 21

Search completed: September 23, 2004, 09:55:36

Job time : 8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 09:57:08 / Search time 6 seconds
(without alignments)
3.656 Million cell updates/sec

Title: US-09-227-881-3
Perfect score: 6169
Sequence: 1 atcttgcagttactctc.....cttgcacctcactgag 6169

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 77 seqs, 1778 residues

Total number of hits satisfying chosen parameters: 154

Minimum DB seq length: 12
Maximum DB seq length: 250

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 78 summaries

Database: rn13.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	3.7	227	US-09-306-828-38	Sequence 38, Appl
2	29	0.5	29	US-08-822-999-8	Sequence 8, Appl
3	29	0.5	29	US-09-056-285A-11	Sequence 11, Appl
4	28	0.5	28	US-08-222-177A-451	Sequence 451, App
5	27	0.4	27	US-08-455-627-23	Sequence 23, Appl
6	27	0.4	27	US-08-222-177A-143	Sequence 143, App
7	27	0.4	27	US-08-689-856-23	Sequence 23, Appl
8	25	0.4	25	US-08-222-177A-146	Sequence 146, App
9	25	0.4	25	US-08-222-177A-145	Sequence 445, App
10	24	0.4	24	US-08-222-177A-454	Sequence 454, App
11	23	0.4	23	US-08-787-321-22	Sequence 22, Appl
12	23	0.4	23	US-09-306-828-38	Sequence 38, Appl
13	22	0.4	22	US-08-222-177A-125	Sequence 125, App
14	22	0.4	22	US-08-222-177A-160	Sequence 160, App
15	21	0.3	21	US-08-529-878B-9	Sequence 9, Appl
16	21	0.3	21	US-08-938-669A-8	Sequence 8, Appl
17	21	0.3	21	US-08-938-669A-12	Sequence 12, Appl
18	21	0.3	21	US-09-306-828-8	Sequence 8, Appl
19	21	0.3	21	US-09-306-828-12	Sequence 12, Appl
20	21	0.3	21	US-08-663-639A-22	Sequence 32, Appl
21	20	0.3	20	US-09-407-675-5	Sequence 5, Appl
22	20	0.3	20	US-08-938-669A-7	Sequence 7, Appl
23	20	0.3	20	US-08-938-669A-9	Sequence 9, Appl
24	20	0.3	20	US-08-938-669A-10	Sequence 10, Appl
25	20	0.3	20	US-08-938-669A-13	Sequence 13, Appl
26	20	0.3	20	US-08-938-669A-19	Sequence 19, Appl
27	20	0.3	20	US-09-488-671-88	Sequence 88, Appl
28	20	0.3	20	US-09-467-642-73	Sequence 73, Appl
29	20	0.3	20	US-09-180-903-8	Sequence 8, Appl
30	20	0.3	20	US-09-056-285A-16	Sequence 16, Appl
31	20	0.3	20	US-09-056-285A-20	Sequence 20, Appl
32	20	0.3	20	US-09-056-285A-21	Sequence 21, Appl
33	20	0.3	20	US-09-056-285A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-306-828-38
Sequence 38, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
TITLE OF INVENTION: Nucleic Acid, Kits, And Methods For The Diagnosis, Prognosis
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/227, 881
EARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 38
LENGTH: 227
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-38
Query Match 3.7%, Score 227, DB 1, Length 227;

Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5045 AACTATTATGGGGATGAGTGCATTAATTTGGAGTGTCTTTTAAAGAACTCCAAA 5104
Db 1 AACTATTATGGGGATGAGTGCATTAATTTGGAGTGTCTTTTAAAGAACTCCAAA 60

QY 5105 CAGACTTCTGGAAGTTATTTCTTAAGAAATCTTCTGGACGCGTGAAGGAAACCCCTG 5164

Db 61 CAGACTTCTGGAAGTTATTTCTTAAGAAATCTTCTGGACGCGTGAAGGAAACCCCTG 120

QY 5165 TGCAAGCCGCCACCCAGCCTCAGCGGACCTCTGTCTTCCCATGAAGAGGCTGCTC 5224

Db 121 TGCAAGCCGCCACCCAGCCTCAGCGGACCTCTGTCTTCCCATGAAGAGGCTGCTC 180

QY 5225 CCCAGTATATATAAACCCTCTCTGAGCTCGGCGCATGAGCCAGCAAG 5271

Db 181 CCCAGTATATATAAACCCTCTCTGAGCTCGGCGCATGAGCCAGCAAG 227

RESULT 2

US-08-822-999-8
; Sequence 8, Application US/08822999
; Patent No. 6271026

GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
TITLE OF INVENTION: GLAUCOMA COMPOSITIONS AND THERAPEUTIC
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,999
FILING DATE: 21-MAR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,347
FILING DATE: 30-JAN-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/748,479
FILING DATE: 08-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,218
FILING DATE: 28-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-822-999-8

Query Match 0.5%; Score 29; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGCTGCAGAGGAGCTGGGACCCCTG 5708
Db 1 AGGGCTGCAGAGGAGCTGGGACCCCTG 29

RESULT 3

US-03-056-285A-11
; Sequence 11, Application US/09056285A
; Patent No. 6403307

GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-03-056-285A-11

Query Match

Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGCTGCAGAGGAGCTGGGACCCCTG 5708
Db 1 AGGGCTGCAGAGGAGCTGGGACCCCTG 29

RESULT 4

US-08-222-177A-451/C
; Sequence 451, Application US/08222177A
; Patent No. 5582979

GENERAL INFORMATION:

APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n, (dg-dt)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison


```

      / INFORMATION FOR SEQ ID NO: 23:
      / SEQUENCE CHARACTERISTICS:
      / LENGTH: 27 nucleotides
      / TYPE: nucleic acid
      / STRANDEDNESS: single
      / TOPOLOGY: linear
      / MOLECULE TYPE: DNA
      / US-08-455-627-23

Query Match          0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy   4996 GTGTGTCGTGTCGTGTCGTGTCGTG 5022
     |||||
Db    27 GTGTGTCGTGTCGTGTCGTGTCGTGTCG 1


RESULT 6
US-08-222-177A-143/c
Sequence 143, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITILE OR INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222.177A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd3lrs
US-08-222-177A-143

Query Match          0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy   4997 TGTGTGTCGTGTCGTGTCGTGTCGTGTCGT 5023
     |||||
Db    27 TGCTGTGTCGTGTCGTGTCGTGTCGTGTCGT 1

```

[illegible][illegible]

Page 5

```

      FILING DATE:
      CLASSIFICATION: 435
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/341,562
      FILING DATE: 21-APR-1989
      ATTORNEY/AGENT INFORMATION:
      NAME: Sara, Charles S.
      REGISTRATION NUMBER: 30,492
      REFERENCE/DOCKET NUMBER: 09865,601
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (608) 831-2100
      TELEFAX: (608) 831-2106
      TELEX:
      INFORMATION FOR SEQ ID NO: 454:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 23 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: DNA (genomic)
      US-08-222-177A-454

Query Match
Best Local Similarity 100.0%, Pred. No. 15,
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTGT 5019
|||||
Db 23 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 12
US-08-787-321-22/c
Sequence 22, Application US/08787321A
Patent No. 6180777
GENERAL INFORMATION:
APPLICANT: Horn, Thomas
TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
FILE REFERENCE: (1300)-1199,002
CURRENT APPLICATION NUMBER: US/08/787,321A
EARLIER FILING DATE: 1997-01-03
EARLIER APPLICATION NUMBER: US PROV 60/009,918
EARLIER FILING DATE: 1996-01-12
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 22
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-08-787-321-22

Query Match
Best Local Similarity 100.0%, Pred. No. 15,
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTG 5018
|||||
Db 23 GTGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 13
US-09-306-828-38/c
Sequence 38, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis

```

CURRENT APPLICATION NUMBER: US/09/306,828
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/227,881
EARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 38
LENGTH: 227
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-38

Query Match 0.4%; Score 22.4; DB 1; Length 227;
Best Local Similarity 81.2%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5073 TTGGATGTTCTTTTAAAGAAACTCCAA 5104
DB 60 TTTGAGTTCTTTTAAAGAACTCCAA 29

RESULT 14
US-08-222-177A-125/c
Sequence 125, Application US/08222177A
Patent No. 5582979

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demilt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.

REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:

INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd25ts
US-08-222-177A-125

Query Match 0.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 5017

DB 22 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 15
US-08-222-177A-160/c
Sequence 160, Application US/08222177A
Patent No. 5582979

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demilt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.

REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:

INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd37rs
US-08-222-177A-160

Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5017
DB 21 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 16
US-08-529-878B-9
Sequence 9, Application US/08529878B
Patent No. 5932556
GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra


```
RESULT 19
US-09-306-828-8/c
; Sequence 8, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-8

Query Match          0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5047 CTATTATTGGGGTATGGGTGC 5067
DB      21 CTATTATTGGGGTATGGGTGC 1

RESULT 20
US-09-306-828-12/c
; Sequence 12, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-12

Query Match          0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4394 CAGTGTGGCAGATACGTTGT 4414
DB      21 CAGTGTGGCAGATACGTTGT 1

RESULT 21
US-08-863-639A-32/c
; Sequence 32, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
```

```
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Wak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueeth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-32

Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4996 GTGTGTGTGTGTGTGTGTGT 5015
DB      20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 22
US-09-407-675-5/c
; Sequence 5, Application US/09407675
; Patent No. 6169176
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas C.
; APPLICANT: Arya, Dev P.
; TITLE OF INVENTION: DEOXYNUCLEIC ALKYL THIUREA COMPOUNDS AND USES THEREOF
; FILE REFERENCE: 30448.65US02
; CURRENT APPLICATION NUMBER: US/09/407,675
; CURRENT FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 09/347,443
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/091,481
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/111,800
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligo 5
US-09-407-675-5

Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-10

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4581 CTGAGAGAGTTCCTCCAGAT 4600
DB 20 CTGAGAGAGTTCCTCCAGAT 1

RESULT 26
US-08-938-669A-13
Sequence 13, Application US/08938669A
Patent No. 6171788
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-13

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3933 TCAGGCTTACTGCAGACC 3952
DB 1 TCAGGCTTACTGCAGACC 20

RESULT 27
US-08-938-669A-19
Sequence 19, Application US/08938669A
Patent No. 6171788
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-19

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5643 ACCTTGACCGAGCTCCGAG 5662
DB 1 ACCTTGACCGAGCTCCGAG 20

RESULT 28
US-08-488-671-88/C
Sequence 88, Application US/09488671A
Patent No. 6187545
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyatt
APPLICANT: Lex M. Cosert
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
FILE REFERENCE: RTS-0123

schul tz881-3.rni

Page 11

Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 24;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	4996	GTGTGTGTGTGTGTGT	5013
Db	20	GTGTGTGTGTGTGTGT	1

```

RESULT 29
US-09-467-642-73/c
; Sequence 73, Application US/09467642
; Patent No. 6300132
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2 EXPRESSION
; FILE REFERENCE: RPS-0106
; CURRENT APPLICATION NUMBER: US/09/467,642
; CURRENT FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-642-73

```

Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. Nc. 24;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      1513 TGCTGGATTACAGGCATGA 1532
          |||||
Db       20  TGCTGGATTACAGGCATGA 1
```

RESULT 30
US-09-180-903-8
; Sequence 8, Application US/09180903

GENERAL INFORMATION:
APPLICANT: Rein, Alan

Henderson, Louis E.
TITLE OF INVENTION: Oligonucleotides Which Specifically Bind
Retroviral Nucleocapsid Proteins

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: ;
; ;

ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California

COUNTRY: USA
STATE: CALIFORNIA
ZIP: 94111-3834

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY

```

;
; MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
;

```

```

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180, 903
FILING DATE: 12-Jul-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,128
FILING DATE: 20-MAY-1996
APPLICATION NUMBER: WO PCT/US97/08936
FILING DATE: 19-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Kathleen L.
REGISTRATION NUMBER: 43,433
REFERENCE/DOCKET NUMBER: :015280-279100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
--S-09-180-903-8

```

```

Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4997 TGTGTGTGTGTGTGTGTG 5016
db 1 TGTGTGTGTGTGTGTGTG 20

```

RESULT 31
US-09-056-285A-16
; Sequence 16, Application US/09056285A
; Patent No. 6403307

```

;
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
;

```

Alward, Wallace L.M.
Fingert, John

TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: EOTEV HOAG & ELLIOT LLP

ADDRESS: 1001, MONROE & 22ND ST.
STREET: One Post Office Square
CITY: Boston

STATE: MA
COUNTRY: USA

ZIP: 02109-2170
COMPUTER READABLE FORM

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-

```

SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/C
FILING DATE: 07-Apr-1998

ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430
REFERENCE / DOCKET NUMBER: HTD-010 38

REFERENCE/DOC#1 NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 011 000 1000

TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000

```

; INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

```

LENGTH: 20 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-056-285A-16

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5216 GGCTGGCTCCCGAGTATATA 5235
DB 1 GGCTGGCTCCCGAGTATATA 20

RESULT 32
US-09-056-285A-20
Sequence 20, Application US/09056285A
Patent No. 6403307
GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-056-285A-20

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5466 AGTGCCGATGCCAGTATAC 5485
DB 1 AGTGCCGATGCCAGTATAC 20

RESULT 33
US-09-056-285A-21/c
Sequence 21, Application US/09056285A
Patent No. 6403307

GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-056-285A-21

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5635 ACCAATTGACCTTGACCGAG 5654
DB 20 ACCAATTGACCTTGACCGAG 1

RESULT 34
US-09-056-285A-22

Sequence 22, Application US/09056285A
Patent No. 6403307

GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John

TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-056-285A-22

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5533 AGCCCATGTCAGTCATCCAT 5552
DB 1 AGCCCATGTCAGTCATCCAT 20

RESULT 35
US-09-056-285A-23/c
Sequence 23, Application US/09056285A
Patent No. 6403307
GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-056-285A-23

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5727 CTGGAACCCCAACCCAGGA 5746
DB 20 CTGGAACCCCAACCCAGGA 1

RESULT 36
US-09-056-285A-25/c
Sequence 25, Application US/09056285A
Patent No. 6403307
GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-056-285A-25

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5821 AAAATGAGATCTGCCGAG 5840
DB 20 AAAATGAGATCTGCCGAG 1

RESULT 37
US-09-056-285A-26
Sequence 26, Application US/09056285A
Patent No. 6403307
GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HONG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-056-285A-26
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5791 TGGAGAGAGAGAGAGCGA 5810
Db 1 TGGAGAGAGAGAGAGCGA 20
RESULT 38
US-09-056-285A-27/c
Sequence 27, Application US/09056285A
Patent No. 6403307
GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.W.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HONG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-056-285A-27
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5958 GGGGACTCTGAGTTGACGAG 5977
Db 20 GGGGACTCTGAGTTGACGAG 1
RESULT 39
US-09-780-175-25/c
Sequence 25, Application US/09780175
Patent No. 6440738
GENERAL INFORMATION:
APPLICANT: Robert McKay
Freier
APPLICANT: Susan M. Freier
Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
FILE REFERENCE: RTS-0164
CURRENT APPLICATION NUMBER: US/09/780,175
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 25
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-175-25
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1340 TCTGCTCCCGAGGTTCAGC 1359
Db 20 TCTGCTCCCGAGGTTCAGC 1
RESULT 40
US-09-607-529-3/c
Sequence 3, Application US/09607529
Patent No. 6465247
GENERAL INFORMATION:
APPLICANT: Irving Weissman
David Traver
APPLICANT: Koichi Akashi
TITLE OF INVENTION: MAMMALIAN MYELOID PROGENITOR CELL
SUBSETS
FILE REFERENCE: STAN-126
CURRENT APPLICATION NUMBER: US/09/607,529
CURRENT FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 60/141,421
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens

US-09-607-523-3

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1511 AGTGTGGATTACAGGCAT 1530
DB 20 AGTGTGGATTACAGGCAT 1

RESULT 41
US-09-306-828-7
Sequence 7, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
CURRENT APPLICATION NUMBER: US/09/306,828
EARLIER FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-7

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4955 TGAATCAGCACCCAGTAG 4974
DB 1 TGAATCAGCACCCAGTAG 20

RESULT 42
US-09-306-828-9
Sequence 9, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
CURRENT APPLICATION NUMBER: US/09/306,828
EARLIER FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 9
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-9

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4587 AGAGTCCCCAGATTACACC 4606
DB 1 AGAGTCCCCAGATTACACC 20

RESULT 43

US-09-306-828-10/C
Sequence 10, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
CURRENT APPLICATION NUMBER: US/09/306,828
EARLIER FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-10

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4581 CTGAGAGAGTCCCCAGAT 4600
DB 20 CTGAGAGAGTCCCCAGAT 1

RESULT 44

US-09-306-828-13
Sequence 13, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
CURRENT APPLICATION NUMBER: US/09/306,828
EARLIER FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 13
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-13

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3933 TCAGGCTTAAGTCAGAAC 3952
DB 1 TCAGGCTTAAGTCAGAAC 20

RESULT 45

US-09-306-828-19
Sequence 19, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
CURRENT APPLICATION NUMBER: US/09/306,828

CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/227,881
EARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO: 19
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-19

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5643 ACCTTGACCGCTGCAG 5662
DB 1 ACCTTGACCGCTGCAG 20

RESULT 46
US-09-060-299-257/c
Sequence 257, Application US/09060299
Patent No. 6545137
GENERAL INFORMATION:
APPLICANT: Todd, John A
APPLICANT: Hess, John W
APPLICANT: Caskey, Charles T
APPLICANT: Cox, Roger D
APPLICANT: Gerhold, David
APPLICANT: Hammond, Holly
APPLICANT: Hey, Patricia
APPLICANT: Kawaguchi, Yoshiniko
APPLICANT: Merriman, Tony R
APPLICANT: Metzker, Michael L
TITLE OF INVENTION: No. 6545137el Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,299
FILING DATE: 15-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J. Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 257:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-060-299-257

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1511 AGTCTGGATTACAGCAT 1530
DB 20 AGTCTGGATTACAGCAT 1

RESULT 47
US-09-402-923A-257/c
Sequence 257, Application US/09402923A
Patent No. 6555654
GENERAL INFORMATION:
APPLICANT: Todd, John A
APPLICANT: Hess, John W
APPLICANT: Caskey, Charles T
APPLICANT: Cox, Roger D
APPLICANT: Gerhold, David
APPLICANT: Hammond, Holly
APPLICANT: Hey, Patricia
APPLICANT: Kawaguchi, Yoshiniko
APPLICANT: Merriman, Tony R
APPLICANT: Metzker, Michael L
TITLE OF INVENTION: No. 6555654el LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01102
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J. Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 257:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 257:
US-09-402-923A-257

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1511 AGTCTGGATTACAGCAT 1530
DB 20 AGTCTGGATTACAGCAT 1

RESULT 48
US-08-222-177A-442/C
Sequence 442, Application US/08222177A
Patent No. 5562979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n (dg-dt)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Rose & Stevens, S.C.
STREET: 8000 Excelstor Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865,601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 442:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-222-177A-442
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGT 5015
DB 19 TGTGTGTGTGTGTGTGT 1

RESULT 49
US-08-629-939-10
Sequence 10, Application US/08629939
Patent No. 5645995
GENERAL INFORMATION:
APPLICANT: Kieback, Dirk G.
TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED
TITLE OF INVENTION: RISK OF BREAST OR OVARIAN CANCER
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MIOW, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,939
FILING DATE: 12-APRIL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-629-939-10
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 AAAGTCTGGATTACAG 1527
DB 1 AAAGTCTGGATTACAG 19

RESULT 50
US-08-759-873-10
Sequence 10, Application US/08759873
Patent No. 5683865
GENERAL INFORMATION:
APPLICANT: Kieback, Dirk G.
TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED RISK
TITLE OF INVENTION: OF BREAST OR OVARIAN CANCER
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MIOW, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,873
FILING DATE: 12-APRIL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-759-873-10

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1509 AAGTGTGGATTACAG 1527
DB 1 AAGTGTGGATTACAG 19

RESULT 51
US-08-915-609-3/c
; Sequence 3, Application US/08915609
; Patent No. 6054300
; GENERAL INFORMATION:
; APPLICANT: McKendree Jr., William L.
; TITLE OF INVENTION: Single-Site Amplification (SSA) Method for Accelerated
; FILE REFERENCE: 0115.97
; CURRENT FILING DATE: 1997-08-21
; EARLIER FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO: 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: primer bind
; LOCATION: (1)..(19)
; NAME/KEY: primer bind
; LOCATION: (1)..(19)
US-08-915-609-3

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4996 GTGTGTGTGTGTGTGTG 5014
DB 19 GTGTGTGTGTGTGTGTG 1

RESULT 52
US-08-915-609-4
; Sequence 4, Application US/08915609
; Patent No. 6054300
; GENERAL INFORMATION:
; APPLICANT: McKendree Jr., William L.
; TITLE OF INVENTION: Single-Site Amplification (SSA) Method for Accelerated
; FILE REFERENCE: 0115.97
; CURRENT FILING DATE: 1997-08-21
; EARLIER FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO: 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: primer bind
; LOCATION: (1)..(19)
; FEATURE:

NAME/KEY: primer bind
LOCATION: (1)..(19)
US-08-915-609-4

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4996 GTGTGTGTGTGTGTGTG 5014
DB 1 GTGTGTGTGTGTGTGTG 19

RESULT 53
US-08-938-669A-11
; Sequence 11, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
; TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
; TITLE OF INVENTION: RELATED DISEASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,669A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/791,154
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mendelson, Elliot
; REGISTRATION NUMBER: P-42,878
; REFERENCE/DOCKET NUMBER: 07425-0034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-6857
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-938-669A-11

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4392 TACAGTGTGCAGATACG 4410
DB 1 TACAGTGTGCAGATACG 19

RESULT 54
US-08-938-669A-14/c
; Sequence 14, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6657
TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-14
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3936 GGCTTAAGTCAGAACCA 3954
Db 19 GGCTTAAGTCAGAACCA 1
RESULT 55
US-08-938-669A-15
Sequence 15, Application US/08938669A
Patent No. 6171788
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6657
TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-15

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6657
TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-15
Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3727 ACAGACACAGGGCATCC 3745
Db 1 ACAGACACAGGGCATCC 19
RESULT 56
US-08-938-669A-17
Sequence 17, Application US/08938669A
Patent No. 6171788
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6657
TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-17

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5373 CCTGAGATGCCAGCTGTCC 5391
DB 1 CCTGAGATGCCAGCTGTCC 19

RESULT 57

US-08-938-669A-22/c
Sequence 22, Application US/08938669A
Patent No. 6171788

GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
TELEFAX: 202 383-6610
TELEX:

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-22

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5864 GGAGCAAGGCTGAGAGG 5882
DB 19 GGAGCAAGGCTGAGAGG 1

RESULT 58
US-08-938-669A-24/c
Sequence 24, Application US/08938669A
Patent No. 6171788

GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
TELEFAX: 202 383-6610
TELEX:

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-24

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5534 GGCCATGTCAGTCATCAT 5552
DB 19 GGCCATGTCAGTCATCAT 1

RESULT 59
US-09-056-285A-19/c
Sequence 19, Application US/09056285A
Patent No. 6403307

GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.W.
Fingerl, John

TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: POLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/056,285A
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-056-285A-19

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5531 CCAGGCCATGTCATC 5549
DB      19 CCAGGCCATGTCATC 1

RESULT 60
US-09-306-828-11
; Sequence 11, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,861
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-11

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4392 TACAGTTGTTCAGATACG 4410
DB      1 TACAGTTGTTCAGATACG 19

RESULT 61
US-09-306-828-14/C
; Sequence 14, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
```

```
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/227,861
EARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 14
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-14

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3936 GGCTTAAGTCAGAACCAA 3954
DB      19 GGCTTAAGTCAGAACCAA 1

RESULT 62
US-09-306-828-15
; Sequence 15, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,861
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 15
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-15

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3727 AGCAGCACAAGGCAATCC 3745
DB      1 AGCAGCACAAGGCAATCC 19

RESULT 63
US-09-306-828-17
; Sequence 17, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,861
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 17
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-17
```

```

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5373 CCTGAGATGCCAGCTGTC 5391
DB      1 CCTGAGATGCCAGCTGTC 19

RESULT 64
US-09-306-828-22/c
; Sequence 22, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-22

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5864 GGTACGACGCTGAGAAG 5882
DB      19 GGTACGACGCTGAGAAG 1

RESULT 65
US-09-306-828-24/c
; Sequence 24, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-24

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5534 GCCCATGTCATCATCCAT 5552
DB      19 GCCCATGTCATCATCCAT 1

RESULT 66
US-09-306-828-35

```

```

; Sequence 35, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 35
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-35

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5045 AACTATTATGGCGTATGG 5063
DB      1 AACTATTATGGCGTATGG 19

RESULT 67
US-09-306-828-36/c
; Sequence 36, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 36
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-36

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5309 CCAGAGGAGCCTCACCAG 5327
DB      19 CCAGAGGAGCCTCACCAG 1

RESULT 68
US-08-700-530-1/c
; Sequence 1, Application US/08700530
; Patent No. 6315186
; GENERAL INFORMATION:
; APPLICANT: EKINS, Roger P
; TITLE OF INVENTION: Binding assay using binding agents with tail groups
; FILE REFERENCE: 0380-P01180US0
; CURRENT APPLICATION NUMBER: US/08/700,530
; CURRENT FILING DATE: 1996-10-23
; PRIOR APPLICATION NUMBER: PCT/GB95/00521
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: GB 9404709.9

```

PRIOR FILING DATE: 1994-03-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-08-700-530-1

Query Match 0.3%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTG 5014
DB 18 TGTGTGTGTGTGTGTGTG 1

RESULT 69
US-08-700-530-2
Sequence 2, Application US/08700530
Patent No. 6316186
GENERAL INFORMATION:
APPLICANT: EKINS, Roger P
TITLE OF INVENTION: Binding assay using binding agents with tail groups
FILE REFERENCE: 0380-P01180US0
CURRENT APPLICATION NUMBER: US/08/700,530
CURRENT FILING DATE: 1996-10-23
PRIOR APPLICATION NUMBER: PCT/GB95/00521
PRIOR FILING DATE: 1995-03-10
PRIOR APPLICATION NUMBER: GB 9404709.9
PRIOR FILING DATE: 1994-03-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-08-700-530-2

Query Match 0.3%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGT 5013
DB 1 GTGTGTGTGTGTGTGTGT 18

RESULT 70
US-08-976-427-28
Sequence 28, Application US/08976427A
Patent No. 6322968
GENERAL INFORMATION:
APPLICANT: Head, Steven R.
APPLICANT: Geoleit, Philip
APPLICANT: Karn, Jonathan
APPLICANT: Boyce-Jacino, Michael
TITLE OF INVENTION: De No. 63229680 or "Universal" Sequencing Array
FILE REFERENCE: 04990.0049
CURRENT APPLICATION NUMBER: US/08/976,427A
CURRENT FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 18
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic primer
US-08-976-427-28

Query Match 0.3%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTG 5014
DB 1 TGTGTGTGTGTGTGTGTG 18

RESULT 71
US-09-648-312-28
Sequence 28, Application US/09648312
Patent No. 6337188
GENERAL INFORMATION:
APPLICANT: Head, Steven R.
APPLICANT: Geoleit, Philip
APPLICANT: Karn, Jonathan
APPLICANT: Boyce-Jacino, Michael
TITLE OF INVENTION: De No. 63371880 or "Universal" Sequencing Array
FILE REFERENCE: 04990.0049
CURRENT APPLICATION NUMBER: US/09/648,312
CURRENT FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic primer
US-09-648-312-28

Query Match 0.3%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTG 5014
DB 1 TGTGTGTGTGTGTGTGTG 18

RESULT 72
US-09-056-285A-17/c
Sequence 17, Application US/09056285A
Patent No. 6403307
GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESS: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-056-285A-17

Query Match 0.3%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5372 GCGTGGATGCGAGCTGT 5389
DB 18 GCGTGGATGCGAGCTGT 1

RESULT 73
US-09-056-285A-18
Sequence 18, Application US/09056285A
Patent No. 6403307
GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-056-285A-18

Query Match 0.3%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5354 ACCTGCTGCGAGCTTGG 5371
DB 1 ACCTGCTGCGAGCTTGG 18

RESULT 74
US-09-056-285A-24
Sequence 24, Application US/09056285A
Patent No. 6403307
GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-056-285A-24

Query Match 0.3%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5641 TGACCTTGACGAGGCTG 5658
DB 1 TGACCTTGACGAGGCTG 18

RESULT 75
US-08-222-177A-448/c
Sequence 448, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demilt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin

```

;
; COUNTRY: USA
; ZIP: 53717-1914
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/222,177A
;
; FILING DATE:
;
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 07/341,562
;
; FILING DATE: 21-APR-1989
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Sara, Charles S.
;
; REGISTRATION NUMBER: 30,492
;
; REFERENCE/DOCKET NUMBER: 09865,601
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (608) 831-2100
;
; TELEFAX: (608) 831-2106
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 448:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 17 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: double
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
;
; US-08-222-177A-448
;
;
; Query Match 0.3%; Score 17; DB 1; Length 17;
; Best Local Similarity 100.0%; Pred. No. 37;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4997 TGTGTGTGTGTGTGTGT 5013
;
; Db 17 TGTGTGTGTGTGTGTGT 1
;
;
; RESULT 76
;
; US-08-885-126-9
;
; Sequence 9, Application US/08885126A
;
; Patent No. 5955597
;
; GENERAL INFORMATION:
;
; APPLICANT: Arnold, Lyle J.
;
; APPLICANT: Riley, Timothy A.
;
; APPLICANT: Reynolds, Mark A.
;
; APPLICANT: Schwartz, David A.
;
; TITLE OF INVENTION: CHIRALITY ENRICHED SYNTHETIC PHOSPHATE
;
; FILE REFERENCE: GENTA.020FW2
;
; CURRENT APPLICATION NUMBER: US/08/885,126A
;
; CURRENT FILING DATE: 1997-06-30
;
; EARLIER APPLICATION NUMBER: 08/343,018
;
; EARLIER FILING DATE: 1994-11-21
;
; EARLIER APPLICATION NUMBER: 08/154,013
;
; EARLIER FILING DATE: 1993-11-16
;
; NUMBER OF SEQ ID NOS: 22
;
; SOFTWARE: FastSeq for Windows Version 3.0
;
; SEQ ID NO 9
;
; LENGTH: 17
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Chemically synthesized oligomer
;
; US-08-885-126-9
;
;
; Query Match 0.3%; Score 17; DB 1; Length 17;
; Best Local Similarity 100.0%; Pred. No. 37;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5008 GTGTGTGTGTGTGTGT 5024
;
; Db 5008 GTGTGTGTGTGTGTGT 5024
;
;
; RESULT 78
;
; US-09-490-774-11
;
; Sequence 11, Application US/09490774
;
; Patent No. 6262036
;
; GENERAL INFORMATION:
;
; APPLICANT: Arnold Jr., Lyle J
;
; APPLICANT: Reynolds, Mark A
;
; APPLICANT: Reynolds, Mark A
```

QY 5008 GTGTGTGTGTGTGTGT 5024

```

;
; Db 1 GTGTGTGTGTGTGTGT 17
;
;
; RESULT 77
;
; US-08-960-111-11
;
; Sequence 11, Application US/08960111
;
; Patent No. 6060456
;
; GENERAL INFORMATION:
;
; APPLICANT: Arnold Jr., Lyle J
;
; APPLICANT: Reynolds, Mark A
;
; APPLICANT: Giachetti, Christina
;
; TITLE OF INVENTION: Chimeric Oligonucleoside Compounds
;
; NUMBER OF SEQUENCES: 27
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Lyon & Lyon
;
; STREET: 611 West Sixth St.
;
; CITY: Los Angeles
;
; STATE: CA
;
; COUNTRY: U.S.A.
;
; ZIP: 90017
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/960,111
;
; FILING DATE:
;
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/238,177
;
; FILING DATE: 04-MAY-1994
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Meier, Paul H.
;
; REGISTRATION NUMBER: 32,274
;
; REFERENCE/DOCKET NUMBER: 207/174
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 213/489-1600
;
; TELEFAX: 213/955-0440
;
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 11:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 17 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: other nucleic acid
;
; HYPOTHETICAL: no
;
; ANTI-SENSE: yes
;
; FEATURE:
;
; NAME/KEY: GT oligomers 2517-1, 2516-1
;
; IDENTIFICATION METHOD: synthesis experiments
;
; OTHER INFORMATION: complementary to synthetic RNA
;
; OTHER INFORMATION: target
;
; US-08-960-111-11
;
;
; Query Match 0.3%; Score 17; DB 1; Length 17;
; Best Local Similarity 100.0%; Pred. No. 37;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5008 GTGTGTGTGTGTGTGT 5024
;
; Db 1 GTGTGTGTGTGTGTGT 17
;
;
; RESULT 78
;
; US-09-490-774-11
;
; Sequence 11, Application US/09490774
;
; Patent No. 6262036
;
; GENERAL INFORMATION:
;
; APPLICANT: Arnold Jr., Lyle J
;
; APPLICANT: Reynolds, Mark A
;
; APPLICANT: Reynolds, Mark A
```

```

1  APPLICANT: Giachetti, Christina
2  TITLE OF INVENTION: Chimeric Oligonucleoside Compounds
3  NUMBER OF SEQUENCES: 27
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Lyon & Lyon
6  STREET: 611 West Sixth St.
7  CITY: Los Angeles
8  STATE: CA
9  COUNTRY: U.S.A.
10 ZIP: 90017
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.25
17
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/490,774
20 FILING DATE:
21 CLASSIFICATION:
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/960,111
24 FILING DATE:
25 APPLICATION NUMBER: US/08/238,177
26 FILING DATE: 04-MAY-1994
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Meier, Paul H.
29 REGISTRATION NUMBER: 32,274
30 REFERENCE/DOCKET NUMBER: 207/174
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 213/489-1600
33 TELEFAX: 213/955-0440
34
35 INFORMATION FOR SEQ ID NO: 11:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 17 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 MOLECULE TYPE: other nucleic acid
42
43 HYPOTHETICAL: no
44 ANTI-SENSE: yes
45
46 FEATURE:
47 NAME/KEY: GT oligomers 2517-1, 2516-1
48 IDENTIFICATION METHOD: synthesis experiments
49 OTHER INFORMATION: complementary to synthetic RNA
50
51 OTHER INFORMATION: target
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
```

Search completed: September 23, 2004, 09:57:15
Job time : 6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

ALIGNMENTS

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 09:58:51; Search time 4 Seconds

(without alignments)
2,952 Million cell updates/sec

Title: US-09-227-881-3

Sequence: 1 acctgtgtcagttacac.....ctgtgtcccccacatgcag 6169

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 0.5

Searched: 32 segs, 957 residues

Total number of hits satisfying chosen parameters: 64

Minimum DB seq length: 12

Maximum DB seq length: 250

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 33 summaries

Database: rnpb3.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	3.7	227	1	US-10-244-633-38
2	32	0.5	32	1	US-10-017-870-1
3	29	0.5	29	1	US-09-952-464A-11
4	27	0.4	27	1	US-09-735-363A-1
5	27	0.4	27	1	US-09-735-363A-5
6	27	0.4	27	1	US-09-735-363A-66
7	27	0.4	27	1	US-09-263-959-770
8	27	0.4	27	1	US-10-168-327-2
9	24	0.4	24	1	US-09-735-363A-21
10	24	0.4	24	1	US-09-735-363A-22
11	24	0.4	24	1	US-09-776-479-1068
12	24	0.4	24	1	US-09-776-479-1068
13	24	0.4	24	1	US-09-909-317-6
14	24	0.4	24	1	US-10-314-578-1068
15	24	0.4	24	1	US-10-112-653-102
16	24	0.4	24	1	US-10-017-995-1068
17	24	0.4	24	1	US-10-374-307-7
18	24	0.4	24	1	US-10-374-307-12
19	24	0.4	24	1	US-10-244-633-38
20	21	0.3	21	1	US-09-735-363A-19
21	21	0.3	21	1	US-09-735-363A-20
22	21	0.3	21	1	US-09-776-479-907
23	21	0.3	21	1	US-09-776-479-907
24	21	0.3	21	1	US-09-985-637A-4
25	21	0.3	21	1	US-09-985-637A-8
26	21	0.3	21	1	US-10-314-578-907
27	21	0.3	21	1	US-10-112-653-876
28	21	0.3	21	1	US-10-017-995-907
29	21	0.3	21	1	US-10-244-633-8
30	21	0.3	21	1	US-10-244-633-12
31	21	0.3	21	1	US-10-287-226-567
32	21	0.3	21	1	US-10-741-339-4
33	21	0.3	21	1	US-10-741-339-8

RESULT 1
US-10-244-633-38
; Sequence 38, Application US/10244633
; Publication No. US20030068640A1
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pa
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244.633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306.828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227.881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 38
; LENGTH: 227
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-38

Query Match 3.7%; Score 227; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 2, 1e-16;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5045 AACTATTATTTGGGGTATGGGTGATTAATTTGGGATGTTCTTTTAAAGAACTCCAA 5104
DB 1 AACTATTATTTGGGGTATGGGTGATTAATTTGGGATGTTCTTTTAAAGAACTCCAA 60
QY 5105 CAGACTTCGAGAGTATTTCTTAAGATCTGTGTCAGCGTGAAGCAACCCCTG 5164
DB 61 CAGACTTCGAGAGTATTTCTTAAGATCTGTGTCAGCGTGAAGCAACCCCTG 120
QY 5165 TGCACAGCCCAACCAAGCCTCAAGTGCACCTCTGTCTTCCCATGAAGGGCTGCTC 5224
DB 121 TGCACAGCCCAACCAAGCCTCAAGTGCACCTCTGTCTTCCCATGAAGGGCTGCTC 180
QY 5225 CCGAGTATATTAACCTCTGAGCTCGGCGATGAGCCAGG 5271
DB 181 CCGAGTATATTAACCTCTGAGCTCGGCGATGAGCCAGG 227
RESULT 2
US-10-017-870-1
; Sequence 1, Application US/10017870
; Publication No. US20030165857A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
; FILE REFERENCE: 034827-1401
; CURRENT APPLICATION NUMBER: US/10/017.870
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-017-870-1

Query Match 0.5%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4305 CGAATGAGCCCTAAACTCAAAAGTGTATATA 4336
1 CGAATGAGCCCTAAACTCAAAAGTGTATATA 32

Db

RESULT 3
US-09-952-464A-11
; Sequence 11, Application US/09952464A
; Publication No. US2003007587A1
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Fingert, John
; TITLE OF INVENTION: GLUCOCMA THERAPEUTICS AND DIAGNOSTICS
; FILE REFERENCE: 21087,0017011
; CURRENT APPLICATION NUMBER: US/09/952,464A
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/473,273
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 09/461,542
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 09/366,952
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 09/056,285
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/822,999
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. US2003007587A1 =
US-09-952-464A-11

Query Match 0.5%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGGCTGAGAGGAGCTGGGACCCCTG 5708
1 AGGGGCTGAGAGGAGCTGGGACCCCTG 29

Db

RESULT 4
US-09-735-363A-1
; Sequence 1, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-1

Query Match 0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5022
1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 27

Db

RESULT 5
US-09-735-363A-5
; Sequence 5, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-5

Query Match 0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5023
1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 27

Db

RESULT 6
US-09-735-363A-66
; Sequence 66, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-66

Query Match 0.4%; Score 27; DB 1; Length 27;

APPLICANT: Phillips, Nigel C.
 APPLICANT: Filion, Mario C.
 TITLE OF INVENTION: Hyaluronic Acid in the Treatment of Cancer
 FILE REFERENCE: 02811-0211 (42368-274915)
 CURRENT APPLICATION NUMBER: US/10/168,327
 CURRENT FILING DATE: 2002-10-07
 PRIOR APPLICATION NUMBER: PCT/CA00/01562
 PRIOR FILING DATE: 2000-12-28
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn version 3.1

```

1 PRIOR APPLICATION NUMBER: 60/2
2 PRIOR FILING DATE: 1999-12-13
3 PRIOR APPLICATION NUMBER: 60/2
4 PRIOR FILING DATE: 2000-08-29
5 NUMBER OF SEQ ID NOS: 87
6 SOFTWARE: PatentIn version 3.0.
7 SEQ ID NO: 22
8 LENGTH: 24
9 TYPE: DNA
10 ORGANISM: Artificial Sequence
11 FEATURE:

```

[illegible]

[illegible]

```
/ PRIOR FILING DATE: 1999-01-11
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: Microsoft Word 97
/ SEQ ID NO 38
/ LENGTH: 227
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-244-633-38

Query Match      0.4%; Score 22.4; DB 1; Length 227;
Best Local Similarity 81.2%; Pred. No. 7.4;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      5073 TTGGAGTGTCTTTTAAAGAACTCCAA 5104
DB      60 TTGGAGTGTCTTTTAAAGAACTCCAA 29

RESULT 20
US-09-735-363A-19
/ Sequence 19, Application US/09735363A
/ Patent No. US20010041681A1
/ GENERAL INFORMATION:
/ APPLICANT: Philip, Mario
/ TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
/ FILE REFERENCE: 02811-0181
/ CURRENT APPLICATION NUMBER: US/09/735,363A
/ PRIOR FILING DATE: 2000-12-12
/ PRIOR APPLICATION NUMBER: 60/170,325
/ PRIOR FILING DATE: 1999-12-13
/ PRIOR APPLICATION NUMBER: 60/226,925
/ PRIOR FILING DATE: 2000-08-29
/ NUMBER OF SEQ ID NOS: 87
/ SOFTWARE: Patent version 3.0
/ SEQ ID NO 19
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-19

Query Match      0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4997 TGTGTGTGTGTGTGTGTGTGT 5017
DB      1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 21
US-09-735-363A-20
/ Sequence 20, Application US/09735363A
/ Patent No. US20010041681A1
/ GENERAL INFORMATION:
/ APPLICANT: Philip, Mario
/ TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
/ FILE REFERENCE: 02811-0181
/ CURRENT APPLICATION NUMBER: US/09/735,363A
/ PRIOR FILING DATE: 2000-12-12
/ PRIOR APPLICATION NUMBER: 60/170,325
/ PRIOR FILING DATE: 1999-12-13
/ PRIOR APPLICATION NUMBER: 60/226,925
/ PRIOR FILING DATE: 2000-08-29
/ NUMBER OF SEQ ID NOS: 87
/ SOFTWARE: Patent version 3.0
/ SEQ ID NO 20
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-20

Query Match      0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4996 GTGTGTGTGTGTGTGTGTGT 5016
DB      1 GTGTGTGTGTGTGTGTGTGT 21

RESULT 22
US-09-776-479-907
/ Sequence 907, Application US/09776479
/ Publication No. US20030087848A1
/ GENERAL INFORMATION:
/ APPLICANT: Bratzler, Robert L.
/ APPLICANT: Petersen, Deanna M.
/ APPLICANT: Fournon, Yves
/ TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
/ FILE REFERENCE: C1037/7013 (HCL/MAT)
/ CURRENT APPLICATION NUMBER: US/09/776,479
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: US 60/179,991
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 1093
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 907
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Sequence
US-09-776-479-907

Query Match      0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4997 TGTGTGTGTGTGTGTGTGTGT 5017
DB      1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 23
US-09-776-479-907
/ Sequence 907, Application US/09776479
/ Publication No. US20040067902A9
/ GENERAL INFORMATION:
/ APPLICANT: Bratzler, Robert L.
/ APPLICANT: Petersen, Deanna M.
/ APPLICANT: Fournon, Yves
/ TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
/ FILE REFERENCE: C1037/7013 (HCL/MAT)
/ CURRENT APPLICATION NUMBER: US/09/776,479
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: US 60/179,991
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 1093
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 907
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Sequence
US-09-776-479-907

Query Match      0.3%; Score 21; DB 1; Length 21;
```

RESULT 26
US-10-314-578-907
; Sequence 907, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:

RESULT 28
US-10-017-995-907
; Sequence 907, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/77025 (HCL/MAT)

Thu Sep 23 10:01:07 2004

schultz881-3.rnpb

Page 9

```

; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 567
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-287-226-567

Query Match      0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1470 AACTCCTGACCTCAGGTGATC 1490
Db      1 AACTCCTGACCTCAGGTGATC 21
```

```

RESULT 32
US-10-741-339-4/c
; Sequence 4, Application US/10741339
; Publication No. US20040132795A1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PRO
; FILE REFERENCE: 13587.375
; CURRENT APPLICATION NUMBER: US/10/741,339
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 09/985,637
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: synthetic
US-10-741-339-4
```

```

Query Match      0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5047 CTATTATGGGGTATGGTGC 5067
Db      21 CTATTATGGGGTATGGTGC 1
```

```

RESULT 33
US-10-741-339-8/c
; Sequence 8, Application US/10741339
; Publication No. US20040132795A1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PRO
; TITLE OF INVENTION: TO DEVELOP GLAUCOMA
```

```

; FILE REFERENCE: 13587.375
; CURRENT APPLICATION NUMBER: US/10/741,339
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 09/985,637
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: synthetic
US-10-741-339-8
```

```

Query Match      0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4394 CAGTGTGCGAGATACGTTGT 4414
Db      21 CAGTGTGCGAGATACGTTGT 1
```

Search completed: September 23, 2004, 09:58:55
Job time : 4 secs

This Page Blank (uspto)

Thu Sep 23 10:01:07 2004

schultz881-3.rnps

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 10:00:21; Search time 2 seconds
(without alignments)
3.788 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169
Sequence: 1 attctgttcagttaccctc.....cttgccccccatgcacg 6169

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 4 secs, 614 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 12

Maximum DB seq length: 250

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 4 summaries

Database: rnps3.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	3.7	227	US-10-244-633-38	Sequence 38, Appl
2	129	2.1	129	US-09-075-126-3026	Sequence 3026, Ap
3	129	2.1	129	US-09-540-208-11923	Sequence 11923, A
4	129	2.1	129	US-60-048-726-3026	Sequence 3026, Ap

ALIGNMENTS

RESULT 1
US-10-244-633-38
Sequence 38, Application US/10244633
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Hu
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
Title Of Invention: Prognosis And Treatment Of Glioma And Related
TITLE OF INVENTION: Disorders
FILE REFERENCE: 07425.0057.US01
CURRENT APPLICATION NUMBER: US/10/244,633
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US/09/306,828
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/227,881
PRIOR FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 38
LENGTH: 227
TYPE: DNA
ORGANISM: Homo sapiens

US-10-244-633-38

Query Match 3.7%; Score 227; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5045 AACTATTATGGGGATGGGTCATTAATGGGATGTTCTTTTAAAGAACTCCAAA 5104
DB 1 AACTATTATGGGGATGGGTCATTAATGGGATGTTCTTTTAAAGAACTCCAAA 60
QY 5105 CAGACTTCTGGAAGGTTATTTTCTAAGATCTTGCTGACCGCTGAGGCAACCCCTG 5164
DB 61 CAGACTTCTGGAAGGTTATTTTCTAAGATCTTGCTGACCGCTGAGGCAACCCCTG 120
QY 5165 TGCACAGCCCAACCCAGCCTCAGCGCCACCTGCTTCCCCATGAGGCTGCTC 5224
DB 121 TGCACAGCCCAACCCAGCCTCAGCGCCACCTGCTTCCCCATGAGGCTGCTC 180
QY 5225 CCCAGTATATATAAACCCTCTGAGCTCGGGCATGAGCCAGCAAG 5271
DB 181 CCCAGTATATATAAACCCTCTGAGCTCGGGCATGAGCCAGCAAG 227

RESULT 2
US-09-075-126-3026
Sequence 3026, Application US/09075126
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: HUMAN PENIS
NUMBER OF SEQUENCES: 3727
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,126
FILING DATE: HERewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0375P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 3026:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 3207049H1
US-09-075-126-3026
Query Match 2.1%; Score 129; DB 1; Length 129;

Thu Sep 23 10:01:06 2004

schultz881-3.rge

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 09:53:56 ; Search time 4 seconds

(without alignments)
3.637 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169

Sequence: 1 atctgtgtcagttaccc.....ctgtgtccctcatgtcag 6169

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 30 segs, 1179 residues

Total number of hits satisfying chosen parameters: 60

Minimum DB seg length: 12

Maximum DB seg length: 250

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 32 summaries

Database : rge3.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	3.7	227	1	BD237965
2	227	3.7	227	1	AR242775
3	29	0.5	29	1	AR163703
4	29	0.5	29	1	AR212952
5	29	0.5	29	1	BD009314
6	29	0.5	29	1	BD225254
7	28	0.5	28	1	I31539
8	27	0.4	27	1	AR051255
9	27	0.4	27	1	AR127802
10	27	0.4	27	1	I28384
11	27	0.4	27	1	I31231
12	27	0.4	27	1	AX175237
13	27	0.4	27	1	AX175241
14	27	0.4	27	1	AX175302
15	27	0.4	27	1	AX189457
16	26	0.4	26	1	BD103417
17	26	0.4	26	1	BD176939
18	25	0.4	25	1	I31234
19	25	0.4	25	1	AX115976
20	25	0.4	25	1	AX117836
21	25	0.4	25	1	BD103418
22	25	0.4	25	1	BD176940
23	24	0.4	24	1	I31533
24	24	0.4	24	1	AX104876
25	24	0.4	24	1	AX175257
26	24	0.4	24	1	AX175258
27	24	0.4	24	1	AX547929
28	23	0.4	23	1	AR127801
29	23	0.4	23	1	I31542
30	22.4	0.4	227	1	BD237965
31	22.4	0.4	227	1	AR242775
32	22	0.4	22	1	I31213

ALIGNMENTS

RESULT 1	BD237965	227 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD237965				
DEFINITION	Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders.				
ACCESSION	BD237965				
VERSION	BD237965.1				
KEYWORDS	JP 2002534135-A/32.				
SOURCE	JP 2002534135-A/32.				
ORGANISM	Homo sapiens (human)				
REFERENCE	BD237965				
AUTHORS	Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.				
TITLE	1 (bases 1 to 227)				
JOURNAL	Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders				
COMMENT	Patent: JP 2002534135-A 32.15-OCT-2002.				
	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA				
	OS Homo sapiens (human)				
	PN JP 2002534135-A/32				
	PD 15-OCT-2002				
	PF 11-JAN-2000 JP 2000593777				
	PR 11-JAN-1999 US 09/227881.07-MAY-1999 US 09/306828 PI				
	THAI D NGUYEN, JON R POLANSKY, PU CHEN, HUA CHEN PC				
	C12N15/09, A61K31/573, A61K45/00, A61P27/06, C12N1/15, C12N1/19, PC				
	C12N1/21,				
	PC C12N5/10, C12Q1/68, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC				
	Nucleic acids, kits, and methods for the diagnosis, prognosis CC				
	and				
	treatment of glaucoma and related disorders				
CC	Key				
FT	source				
FT	1. 227				
FEATURES	Location/Qualifiers				
source	1. 227				
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
Query Match	3.7%; Score 227; DB 1; Length 227;				
Best Local Similarity	100.0%; Pred. No. 9.3e-16;				
Matches	227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	5045 AACTATTATTTGGGATGATGGTGCATTAATTTGGGATGATGTTTAAAGAACTCCAA 5104				
DB	1 AACTATTATTTGGGATGATGGTGCATTAATTTGGGATGATGTTTAAAGAACTCCAA 60				
OY	5105 CAGACTTGTGAAGGTTATTTCTAAGATCTTGTGTCAGCGTGAAGCAACCCCTG 5164				
DB	61 CAGACTTGTGAAGGTTATTTCTAAGATCTTGTGTCAGCGTGAAGCAACCCCTG 120				
OY	5165 TGACAGCCCCACCCAGCTCACTGTCAGCCCTGTTCCCCCATGAAGGGCTGCTC 5224				
DB	121 TGACAGCCCCACCCAGCTCACTGTCAGCCCTGTTCCCCCATGAAGGGCTGCTC 180				
OY	5225 CCGAGTATATTAACCTCTCTGAGCTCGGCGCAGACCCGAGAG 5271				
DB	181 CCGAGTATATTAACCTCTCTGAGCTCGGCGCAGACCCGAGAG 227				
RESULT 2	AR242775	227 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	AR242775				
DEFINITION	Sequence 38 from patent US 6475724.				
ACCESSION	AR242775				
VERSION	AR242775.1				
KEYWORDS	GI:27289414				
SOURCE	Unknown.				
ORGANISM	Unknown.				

Unclassified.
REFERENCE 1 (bases 1 to 227)
AUTHORS Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders
JOURNAL Patent: US 6475724-A 38 05-NOV-2002;
FEATURES Location/Qualifiers
source 1..227
/organism="unknown"
/mol_type="genomic DNA"

Query Match 3.7%; Score 227; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.3e-16;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5045 AACTATATTTGGGGTATGGGTGCTCAATATTTGGGATGTTCTTTTAAAGAAATCCAAA 5104
DB 1 AACTATATTTGGGGTATGGGTGCTCAATATTTGGGATGTTCTTTTAAAGAAATCCAAA 60
QY 5105 CAGACTTCTGGAAGGTATTTCTTGAAGATCTGTGTGCGACGCGAAGGCAACCCCTCG 5164
DB 61 CAGACTTCTGGAAGGTATTTCTTGAAGATCTGTGTGCGACGCGAAGGCAACCCCTCG 120
QY 5165 TGCACAGCCGCCACCCAGCCTCAAGTGCACCTCTGTCTTCCCATGAAGGGCTGCTC 5224
DB 121 TGCACAGCCGCCACCCAGCCTCAAGTGCACCTCTGTCTTCCCATGAAGGGCTGCTC 180
QY 5225 CCAGATATATTAACCTCTCTGTGAGCTCGGCGCATGAGCCAGAG 5271
DB 181 CCAGATATATTAACCTCTCTGTGAGCTCGGCGCATGAGCCAGAG 227

RESULT 3
LOCUS AR163703 29 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6271026.
ACCESSION AR163703
VERSION AR163703.1 GI:16234393
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Stone,E.M., Sheffield,V.C. and Alward,W.L.M.
TITLE Glaucoma compositions
JOURNAL Patent: US 6271026-A 8 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGGCTGCAGAGGAGCTGGGCAACCTG 5708
DB 1 AGGGGCTGCAGAGGAGCTGGGCAACCTG 29

RESULT 4
LOCUS AR212952 29 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 11 from patent US 6403307.
ACCESSION AR212952
VERSION AR212952.1 GI:23309837
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Stone,E.M., Sheffield,V.C., Alward,W.L.M. and Fingert,J.
TITLE Glaucoma therapeutics and diagnostics

JOURNAL Patent: US 6403307-A 11 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGGCTGCAGAGGAGCTGGGCAACCTG 5708
DB 1 AGGGGCTGCAGAGGAGCTGGGCAACCTG 29

RESULT 5
LOCUS BD009314 29 bp DNA linear PAT 31-JAN-2002
DEFINITION Glaucoma-associated protein and corresponding nucleic acid and their therapeutic and diagnostic uses.
ACCESSION BD009314
VERSION BD009314.1 GI:18637687
KEYWORDS JP 2001503631-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 29)
AUTHORS Stone,E.M., Sheffield,V. and Alward,W.L.M.
TITLE Glaucoma-associated protein and corresponding nucleic acid and their therapeutic and diagnostic uses
JOURNAL Patent: JP 2001503631-A 7 21-MAR-2001;
COMMENT UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS Unidentified
PN JP 2001503631-A/7
PD 21-MAR-2001
PF 07-NOV-1997 JP 1998521884
PR 08-NOV-1996 US 08/748479,30-JAN-1997 US 08/791347 PR
PI 21-MAR-1997 US 08/822299
PI EDWIN M STONE, VAL SHEFFIELD, WALLACE L M ALWARD, PC
C12N15/12, C07K14/47, C07K16/18, A61K39/395, G01N33/53, C12Q1/68, PC
C12N15/11,
PC A61K31/70, A01K67/027
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source 1..29
/organism="Unidentified".
FEATURES Location/Qualifiers
source 1..29
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.5%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGGCTGCAGAGGAGCTGGGCAACCTG 5708
DB 1 AGGGGCTGCAGAGGAGCTGGGCAACCTG 29

RESULT 6
LOCUS BD225254 29 bp DNA linear PAT 17-JUL-2003
DEFINITION Remedies and diagnostic agents of glaucoma.
ACCESSION BD225254
VERSION BD225254.1 GI:33035024
KEYWORDS JP 2002510508-A/9.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 29)
 AUTHORS Stone,E.M., Sheffield,V.C., Alward,W.L.M. and Fingert,J.
 TITLE Remedies and diagnostic agents of glaucoma
 JOURNAL Patent: JP 2002510508-A 9 09-APR-2002;
 THE UNIVERSITY OF IOWA RESEARCH FOUNDATION
 COMMENT OS Homo sapiens (human)
 PN JP 2002510508-A/9
 PD 09-APR-2002
 PF 07-APR-1999 JP 2000542490
 PR 07-APR-1998 US 09/056285
 PI EDWIN M STONE, VAL C SHEPHERD, WALLACE L M ALWARD, JOHN FINGERT
 PC C12N15/09, C12Q1/68, C12N15/00
 CC Remedies and diagnostic agents of glaucoma
 FH Key
 FT Location/Qualifiers
 source 1..29
 /organism='Homo sapiens (human)'
 /location/Qualifiers
 1..29
 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

Query Match 0.5%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGGCTGCAAGAGGAGCTGGGACCCCTG 5708
 DB 1 AGGGGCTGCAAGAGGAGCTGGGACCCCTG 29

RESULT 7
 LOCUS 131539 28 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 451 from patent US 5582979.
 ACCESSION 131539
 VERSION 131539.1 GI:1822330
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Weber,J.L.
 TITLE Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and method of using the same
 JOURNAL Patent: US 5582979-A 451 10-DEC-1996;
 FEATURES Location/Qualifiers
 source 1..28
 /organism='unknown'
 /mol_type='unassigned DNA'

Query Match 0.5%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 5023
 DB 28 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 8
 LOCUS AR051255 27 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 23 from patent US 5830658.
 ACCESSION AR051255
 VERSION AR051255.1 GI:5974619
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Grayzov,S.M.
 TITLE Convergent synthesis of branched and multiply connected

JOURNAL Macromolecular structures
 PATENT: US 5830658-A 23 03-NOV-1998;
 LOCATION/Qualifiers
 source 1..27
 /organism='unknown'
 /mol_type='unassigned DNA'

Query Match 0.4%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 5022
 DB 27 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 9
 LOCUS AR127802 27 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 23 from patent US 6180777.
 ACCESSION AR127802
 VERSION AR127802.1 GI:14114397
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Horn,T.
 TITLE Synthesis of branched nucleic acids
 JOURNAL Patent: US 6180777-A 23 30-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..27
 /organism='unknown'
 /mol_type='unassigned DNA'

Query Match 0.4%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 5022
 DB 27 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 10
 LOCUS 128384 27 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 23 from patent US 5571677.
 ACCESSION 128384
 VERSION 128384.1 GI:1819160
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Grayzov,S.M.
 TITLE Convergent synthesis of branched and multiply connected macromolecular structures
 JOURNAL Patent: US 5571677-A 23 05-NOV-1996;
 FEATURES Location/Qualifiers
 source 1..27
 /organism='unknown'
 /mol_type='unassigned DNA'

Query Match 0.4%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 5022
 DB 27 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 11
LOCUS 131231/c 27 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 143 from patent US 5582979.
ACCESSION 131231
VERSION 131231.1 GI:1822022
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Weber,J.L.
TITLE length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 143 10-DEC-1996;
FEATURES
Source
1..27
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5023
Db 27 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1
RESULT 12
LOCUS AX175237 27 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 1 from Patent WO0144465.
ACCESSION AX175237
VERSION AX175237.1 GI:14596605
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Phillips,N.C. and Pillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 1 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
Source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5022
Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27
RESULT 13
LOCUS AX175241 27 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 5 from Patent WO0144465.
ACCESSION AX175241
VERSION AX175241.1 GI:14598609
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Phillips,N.C. and Pillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 5 21-JUN-2001;

FEATURES
Source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5023
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27
RESULT 14
LOCUS AX175302 27 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 66 from Patent WO0144465.
ACCESSION AX175302
VERSION AX175302.1 GI:14598670
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Phillips,N.C. and Pillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 66 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
Source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5022
Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27
RESULT 15
LOCUS AX189457 27 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 2 from Patent WO0147561.
ACCESSION AX189457
VERSION AX189457.1 GI:15142969
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Phillips,N.C. and Pillion,M.C.
TITLE Hyaluronic acid in the treatment of cancer
JOURNAL Patent: WO 0147561-A 2 05-JUL-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
Source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"
Query Match 0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5022

[illegible][illegible]

```

source
1.24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
0.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGT 5019
DB 1 GTGTGTGTGTGTGTGTGTGT 24

RESULT 27
AX547929 24 bp DNA PAT 01-MAR-2003
LOCUS AX547929
DEFINITION Sequence 1066 from Patent WO02053141.
ACCESSION AX547929
VERSION AX547929.1 GI:25813073
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Bratzler,R.L.
AUTHORS Inhibition of angiogenesis by nucleic acids
TITLE Patent: WO 02053141-A 1068 11-0UL-2002;
JOURNAL Coley Pharmaceutical Group, Inc. (US)
LOCATION/Qualifiers
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match
0.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTG 5020
DB 1 TGTGTGTGTGTGTGTGTGTGTG 24

RESULT 28
AR127801 23 bp DNA linear PAT 16-MAY-2001
LOCUS AR127801/c
DEFINITION Sequence 22 from patent US 6180777.
ACCESSION AR127801
VERSION AR127801.1 GI:14114396
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Horn,T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 22 30-JUN-2001;
FEATURES
location/Qualifiers
1..23
/organism="Unknown"
/mol_type="unassigned DNA"

Query Match
0.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTG 5018
DB 23 GTGTGTGTGTGTGTGTGTGTG 1

```

```

Db 60 TTGGAGTTCTTTTAAAAAGAACATCCCA 29

RESULT 31
AR242775/c 227 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION Sequence 38 from patent US 6475724.
ACCESSION AR242775
VERSION AR242775.1 GI:27289414
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 227)
  Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
  Nucleic acids, kits, and methods for the diagnosis, prognosis and
  treatment of glaucoma and related disorders
  Patent: US 6475724-A 38 05-NOV-2002;
  Location/Qualifiers
    1..227
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match 0.4%; Score 22.4; DB 1; Length 227;
Best Local Similarity 81.2%; Pred. No. 3.7;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5073 TTGGAGTTCTTTTAAAAAGAACATCCCA 5104
Db 60 TTGGAGTTCTTTTAAAAAGAACATCCCA 29

RESULT 32
I31213/c 22 bp DNA linear PAT 06-FEB-1997
LOCUS
DEFINITION Sequence 125 from patent US 5582979.
ACCESSION I31213
VERSION I31213.1 GI:1822004
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 22)
  Weber,J.L.
  Length polymorphisms in (dC-da).sub.n.(dG-dT).sub.n sequences and
  method of using the same
  Patent: US 5582979-A 125 10-DEC-1996;
  Location/Qualifiers
    1..22
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match 0.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4996 GTGTGTGTGTGTGTGTGTGTGT 5017
Db 22 GTGTGTGTGTGTGTGTGTGTGT 1

Search completed: September 23, 2004, 09:54:00
Job time : 4 secs

```